

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 18:59:56 ; Search time 3974.06 Seconds
(without alignments)
16370.617 Million cell updates/sec

Title: US-09-845-416-10_COPY_1500_3000

Perfect score: 1501
Sequence: 1 acaatggcaagacctccaag.....accagcgaggtggcctc 1501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1501	100.0	5339	6	AX538620	AX538620 Sequence
2	1501	100.0	5462	6	AX538621	AX538621 Sequence
3	1501	100.0	5952	6	AR304538	AR304538 Sequence
4	1501	100.0	5952	6	AX114289	AX114289 Sequence
5	1501	100.0	8689	6	AX538622	AX538622 Sequence
6	1501	100.0	11443	6	AX538624	AX538624 Sequence
7	1501	100.0	12057	6	AX538627	AX538627 Sequence
8	1501	100.0	12446	9	HSDMDR	X14298 Human mRNA
9	1501	100.0	13957	6	AX409637	AX409637 Sequence
10	1501	100.0	13957	6	AX538581	AX538581 Sequence
11	1501	100.0	13957	9	HUMDYS	M18533 Homo sapien
12	1497.4	99.8	13977	6	AR220819	AR220819 Sequence
13	1336.2	89.0	13887	4	AF070485	AF070485 Canis fam
14	1298.4	86.5	13815	6	AX306153	AX306153 Sequence
15	1298.4	86.5	13815	6	AX538582	AX538582 Sequence
16	1298.4	86.5	13815	10	MUSDYSA	M68859 Mouse dyst
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ALIGNMENTS

RESULT 1
AX538620

LOCUS AX538620

DEFINITION Sequence 40 from Patent WO0229056.

ACCESSION AX538620

VERSION AX538620.1

KEYWORDS GI:25271166

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE artificial sequences.

AUTHORS 1

TITLE Chamberlain, J.S. and Harper, S.Q.

JOURNAL Mini-dystrophin nucleic acid and peptide sequences

Patent: WO 0229056-A 40 11-APR-2002;

THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)

5339 bp DNA linear PAT 23-NOV-2002

FEATURES		Location/Qualifiers	
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		/mol_type="unassigned DNA"	
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Query Match 100.0%; Score 1501; DB 6; Length 5339;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	61	TGAAAACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA	120
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QY	181	TAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA	240
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QY	241	ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG	300
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QY	361	AACTAAAGAACTGTATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA	420
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QY	421	GCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCAGAGAGCTGCCTCTCTGAGGAGAG	480
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QY	781	TGACCTTGTCTGCCAGCTTACCACCTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCAC	840
Db	2473	TGACCTTGTCTGCCAGCTTACCACCTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCAC	2532
QY	841	TCTGGAAGACCTTGAAACACCAAGATGGAAGCTTCTGACGGTGGCCGTGAGGACCGAGTCAG	900
Db	2533	TCTGGAAGACCTTGAAACACCAAGATGGAAGCTTCTGACGGTGGCCGTGAGGACCGAGTCAG	2592
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QY	1321	TATGTCTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGT	1380
Db	3013	TATGTCTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGT	3072
QY	1381	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	1440
Db	3073	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	3132
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DEFINITION			
Sequence 41 from Patent WO0229056.			
ACCESSION			
AX538621			
VERSION			
AX538621.1 GI:25271168			
KEYWORDS			
SOURCE			
ORGANISM			
synthetic construct			
synthetic construct			
artificial sequences.			
REFERENCE			
1			
AUTHORS			
Chamberlain, J.S. and Harper, S.Q.			
TITLE			
Mini-dystrophin nucleic acid and peptide sequences			
JOURNAL			
Patent: WO 0229056-A 41 11-APR-2002;			
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)			
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/mol_type="unassigned DNA"			
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Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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LOCUS			
DEFINITION			
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QY 1501 C 1501

Db 4602 C 4602

RESULT 4
AX114289
LOCUS AX114289 5952 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1 from Patent WO0129243.
ACCESSION AX114289
VERSION AX114289.1 GI:14031259
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Paul, X.L. and Xiao, X.
TITLE Method and vector for producing and transferring trans-spliced peptides
JOURNAL Patent: WO 0129243-A 1 26-APR-2001;
DALHOUSIE UNIVERSITY (CA); UNIV. OF PITTSBURGH OF THE COMMONWEALTH
SYSTEM OF HIGHER EDUCATION (US)
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misc_feature 2897..2898
/note="S4 junction site"
misc_feature 3198..3199
/note="S2 junction site"
ORIGIN
Query Match 100.0%; Score 1501; DB 6; Length 5952;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGA 60
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QY 61 TGAACACAGCCAAAAATCCTGAGATCCCTGGAAGTTCGATGATGCGAGTCTCTGTAC 120
Db 3162 TGAACACAGCCAAAAATCCTGAGATCCCTGGAAGTTCGATGATGCGAGTCTCTGTAC 3221
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Db 3222 AAGAGCTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAGTCTCTCAACAT 3281
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Db 3402 CGACTTTCCAGCAGTTCCAGAAAGCAGAACCGATGTACATAGGGCTTCAAGAGGGAATTGAA 3461
QY 361 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420

QY	601	CCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTCGGCCAAGCTGAGGTGAT	660
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QY	661	CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACTCGA	720
Db	3808	CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACTCGA	3867
QY	721	GAAGCTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCAA	780
Db	3868	GAAGCTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCAA	3927
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Db	3928	TGACCTTGCTCGCCAGCTTACCATTGCGGCATTGAGCTCTCACCGTATAACCTCAGCAC	3987
QY	841	TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCGCTCGAGGACCGAGTCAG	900
Db	3988	TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCGCTCGAGGACCGAGTCAG	4047
QY	901	GCAGCTGCATGAAGCCCAACAGGACCTTGGTCCAGCATCTCAGCACTTCTTCCACAGTC	960
Db	4048	GCAGCTGCATGAAGCCCAACAGGACCTTGGTCCAGCATCTCAGCACTTCTTCCACAGTC	4107
QY	961	TGTCAGGCTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCA	1020
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QY	1081	TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGACATGAACTCCGAGAGACTGCA	1140
Db	4228	TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGACATGAACTCCGAGAGACTGCA	4287
QY	1141	GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGAGCCTGTGATGCCCTGGACCA	1200
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QY	1261	TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGA	1320
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QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAAGCGGAGGCTGGCCT	1500
Db	4588	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAAGCGGAGGCTGGCCT	4647
QY	1501	C 1501	
Db	4648	C 4648	

RESULT 6
AX538624
LOCUS AX538624 11443 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 44 from Patent WO229056.
ACCESSION AX538624
VERSION AX538624.1 GI:25271175
KEYWORDS
SOURCE synthetic construct

ORGANISM	synthetic construct		
REFERENCE	artificial sequences.		
AUTHORS	Chamberlain, J.S. and Harper, S.Q.		
TITLE	Mini-dystrophin nucleic acid and peptide sequences		
JOURNAL	Patent: WO 0229056-A 44 11-APR-2002;		
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Best Local Similarity	100.0%;	Pred. No. 0;	
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QY	61	TGAAACAGCCAAAAATCCTGAGATCCCTGGAAGTTCCTGATGATGCGTCTCTGTACA	120
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QY	181	TAGTCCCATTTGGAAGCCAGTCTGACCAAGTGGAGCGTCTGCACCTTTCTCTGCAGGA	240
Db	6082	TAGTCCCATTTGGAAGCCAGTCTGACCAAGTGGAGCGTCTGCACCTTTCTCTGCAGGA	6141
QY	241	ACTTCTGCTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGCAGGCACCTATTGGAGG	300
Db	6142	ACTTCTGCTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGCAGGCACCTATTGGAGG	6201
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QY	361	AACTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA	420
Db	6262	AACTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA	6321
QY	421	GCCTTTGGAAGGACTAGAGAAACTCTACAGGAGCCCGAGAGAGCTGCCTCTGAGGAGAG	480
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QY	481	AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA	540
Db	6382	AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA	6441
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Db	6442	AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTTGAAAGACT	6501
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Db	6502	CCAGGAACTTCAAGAGGCCACCGATGAGCTGAGCTCAAGCTCGCCCAAGCTGAGGTGAT	6561
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Db	6562	CAAGGGATCCTGGCAGCCCGTGGCGGATCTCTCATTTGACTCTCTCAAGATCACCTCGA	6621
QY	721	GAAAGTCAAGGCACTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACTGAGCCACGTCAA	780
Db	6622	GAAAGTCAAGGCACTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACTGAGCCACGTCAA	6681
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Db 6742 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTGAGGACCGAGTCAG 6801

QY 901 GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTC 960

Db 6802 GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTC 6861

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Db 7042 GAAGGCCCTTTGCTGGATCTCTTGAGCCCTGTGAGCTGCATGATGCTTGGACCAACA 7101

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Db 7162 TATTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACCTCCCTCTCTGCGTGGGA 7221

QY 1321 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGACAGGGAGGATCCGTGT 1380

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QY 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGCAAGTACAG 1440

Db 7282 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGCAAGTACAG 7341

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QY 1501 C 1501

Db 7402 C 7402

RESULT 7

AX538627

LOCUS AX538627

DEFINITION Sequence 47 from Patent WO0229056.

ACCESSION AX538627

VERSION AX538627.1 GI:25271181

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Chamberlain J.S. and Harper S.O.

TITLE Mini-dystrophin nucleic acid and peptide sequences

JOURNAL Patent: WO 0229056-A 47 11-APR-2002;

THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)

FEATURES

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1. .12057

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/note="Synthetic"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TGAACACAGCCCAAAATCCTGAGATCCCTGGAAGTCCGATGATGCGAGTCTGTACA 120

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QY 121 AAGACGTTTGGATAACATGAATCAAGTGGAGTGAATTCGAAAAAGTCTCTCAACAT 180

Db 8536 AAGACGTTTGGATAACATGAATCAAGTGGAGTGAATTCGAAAAAGTCTCTCAACAT 8595

QY 181 TAGTCCCATTTGGAAGCCAGTTCTGACCAAGTGGAGCGCTCTGCACCTTTCTTCAGGA 240

Db 8596 TAGTCCCATTTGGAAGCCAGTTCTGACCAAGTGGAGCGCTCTGCACCTTTCTTCAGGA 8655

QY 241 ACTTCTGCTGTGGCTACAGTGAAGATGATGAATTAAGCCGCGAGCACTATTGGAGG 300

Db 8656 ACTTCTGCTGTGGCTACAGTGAAGATGATGAATTAAGCCGCGAGCACTATTGGAGG 8715

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Db 8716 CGACTTCCAGCAGTTTCAAGACGAGAACGATGATAGGGCTTCAAGAGGGAATTTGAA 8775

QY 361 AACTAAAGAACCTGTATCATGAGTACTCTTGAAGTGTACGAATATTTCTGACAGAGCA 420

Db 8776 AACTAAAGAACCTGTATCATGAGTACTCTTGAAGTGTACGAATATTTCTGACAGAGCA 8835

QY 421 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCTGAGGAGAG 480

Db 8836 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCTGAGGAGAG 8895

QY 481 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 540

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QY 541 AAAATGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTGAAGACT 600

Db 8956 AAAATGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTGAAGACT 9015

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QY	1021	CGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGC	1080
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QY	1081	TGACCTGAATAATGTCTAGCTTATAGGACTGCGATGAACTCCGAAGACTGCA	1140
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Db	9556	GAAGGCCCTTGTCTGGATCTCTTGAGCCTGTGAGCTGATGATGCTTGGACGACCA	9615
QY	1201	CAACCTCAAGCAAAATGACGACCCATGGATATCCTGCAGATTATTAATTGTTGACCA	1260
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QY	1321	TATGTGTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT	1380
Db	9736	TATGTGTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT	9795
QY	1381	CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	1440
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QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCACAGGATTTTGTGACGACGCGAGGCTGGGCT	1500
Db	9856	ATACCTTTTCAAGCAAGTGGCAAGTTCACAGGATTTTGTGACGACGCGAGGCTGGGCT	9915
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Db	9916	C 9916	

RESULT 8
HSDMDR Human mRNA for dystrophin. 12446 bp mRNA linear PRI 12-SEP-1993

LOCUS X14298
DEFINITION X14298
ACCESSION X14298
VERSION X14298.1 GI:30845
KEYWORDS Dmd gene; Duchenne muscular dystrophy; dystrophin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 12446)
AUTHORS Rosenthal,A., Speer,A., Billwitz,H., Cross,G.S., Forrest,S.M. and Davies,K.E.
Two human cDNA molecules coding for the Duchenne muscular dystrophy (DMD) locus are highly homologous
Nucleic Acids Res. 17 (13), 5391 (1989)
JOURNAL MEDLINE 89345106
PUBMED 2668885
REFERENCE 2 (bases 1 to 12446)
AUTHORS Rosenthal,A.
Direct Submission
Submitted (09-FEB-1989) Rosenthal A., Akademie der Wissenschaften der DDR, Zentralinstitut fuer Molekularbiologie, Robert-Roessle Str.10, 1115 Berlin Buch, DDR
COMMENT See also M18533 and M20250 for Dmd seqs.; discrepancies compared to M18533 cDNA were located at x14298 pos. 496, 1772, 1965, 2449, 3687, 4229, 4504, 5075, 5332, 5630 and 7194.
FEATURES Location/Qualifiers
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ORIGIN

		Query Match	100.0%;	Score 1501;	DB 9;	Length 12446;		
		Best Local Similarity	100.0%;	Pred. No. 0;				
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QY	1	ACAATGGCAAGACCTCCAAAGGTGAAATTAAGCTCACACAGATGTTTATCACAACTGGA	60					
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QY	61	TGAAAAACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCTCTGTTACA	120					
Db	8366	TGAAAAACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCTCTGTTACA	8425					
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Db	8426	AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT	8485					
QY	181	TAGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACTTTCTCTGCAGGA	240					
Db	8486	TAGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACTTTCTCTGCAGGA	8545					
QY	241	ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGCAGGCACCTATTGGAGG	300					
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QY	301	CGACTTTCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA	360					
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QY	421	GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCCGAGAGCTGCCCTCCTGAGGAGAG	480					
Db	8726	GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCCGAGAGCTGCCCTCCTGAGGAGAG	8785					
QY	481	AGCCAGAAATGTCACTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTAGTGGGA	540					
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QY	541	AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGAAGCT	600					
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Db	9806	C 9806						

RESULT 9
AX409637
LOCUS AX409637 13957 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2284 from Patent WO0229103.
ACCESSION AX409637
VERSION AX409637.1 GI:21442342
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 2284 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Db	8476	TGAAAAACAGCCAAAAATCCTGAGATCCCTGGAAAGTTCCGATGATGCAGTCTGTTACA	8535					
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QY 1501 C 1501
Db 9916 C 9916

RESULT 10
AX538581
LOCUS AX538581 13957 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 1 from Patent WO0229056.
ACCESSION AX538581
VERSION AX538581.1 GI:25271086
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chamberlain, J.S. and Harper, S.Q.
TITLE Mini-dystrophin nucleic acid and peptide sequences
JOURNAL Patent: WO 0229056-A 1 11-APR-2002;
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 9916 C 9916
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LOCUS Homo sapiens dystrophin (DMD) mRNA, complete cds.
DEFINITION M18533 M17154 M18026 M20250
ACCESSION M18533.1 GI:181856
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1699)
AUTHORS Koenig,M., Hoffman,E.P., Bertelson,C.J., Monaco,A.P., Feener,C. and Kunkel,L.M.
TITLE Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary genomic organization of the DMD gene in normal and affected individuals
JOURNAL Cell 50 (3), 509-517 (1987)
MEDLINE 87273512
PUBMED 3607877
REFERENCE 2 (bases 1678 to 3830)
AUTHORS Hoffman,E.P., Monaco,A.P., Feener,C.C. and Kunkel,L.M.
TITLE Conservation of the Duchenne muscular dystrophy gene in mice and humans
JOURNAL Science 238 (4825), 347-350 (1987)
MEDLINE 88018015
PUBMED 3659917
REFERENCE 3 (bases 1 to 13957)
AUTHORS Koenig,M., Monaco,A.P. and Kunkel,L.M.
TITLE The complete sequence of dystrophin predicts a rod-shaped cytoskeletal protein
JOURNAL Cell 53 (2), 219-226 (1988)
MEDLINE 88194521
PUBMED 3282674
COMMENT On May 25, 2000 this sequence version replaced gi:340693.
Draft entry and computer-readable sequence kindly provided by M.Koenig, 01-APR-1988 The severity of muscular dystrophy is determined by the size of the deleted DNA segment. Deletions found in different patients were from positions 302-2200, 473-1168, 1691-1810, and 1169-3011.
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ORIGIN

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 Carville,K.S., Mann,C.J., Schatzberg,S.J. and Wilton,S.D.
 Direct Submission
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 Australia, Verdun Street, Nedlands, WA 6018, Australia
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AUTHORS				
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Method for examining ischemic conditions				
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Db	8647	ACTTCTGTGTGGTACAGCTGAAAGATGATGAATTAAGCCGGCAGGAC	CCTATTGGAGG	8706
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Qy	361	AACTAAAGAACCTGTATATCATGAGTACTCTTTGAGACTGTACGAAT	ATTTCTGACAGAGCA	420
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Qy	481	AGCCCAGAAATGTCACTCGCTTCTACGAAAGCAGGCTGAGGAGGTCA	ATACTGAGTGGGA	540
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Qy	601	CCAGAACTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCA	AGCTGAGGTGAT	660
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Qy	781	TGACCTTGCTCGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCG	TATACCTCAGCAC	840
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LOCUS AX538582 13815 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 2 from Patent WO0229056.
ACCESSION AX538582
VERSION AX538582.1 GI:25271088
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Chamberlain, J.S. and Harper, S.Q.
TITLE Mini-dystrophin nucleic acid and peptide sequences
JOURNAL Patent: WO 0229056-A 2 11-APR-2002;
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)
FEATURES
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1. .13815
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 86.5%; Score 1298.4; DB 6; Length 13815;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 1 ACAAATGGCAAGACCTCAAGGTGAAATTTGAGCTCACACAGATGTTATCAACACCTGGA 60

Db 8407 ACCATGGCAAGATCTCCAAGGAGAAATTGAAACTCACACAGATATCTATCACAATCTTGA 8466
QY 61 TGAACACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGACGTCCTGTGTTACA 120
Db 8467 TGAACATGGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGAAAGCACCCCTGTGTTACA 8526
QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGAAAAAAGTCTCTCAACAT 180
Db 8527 AAGACGTTTGGATAACATGAATTTCAAGTGGAGTGAACCTTCGAAAAAAGTCTCTCAACAT 8586
QY 181 TAGGTCCCATTTGGAAAGCCAGTTCTGACCAAGTGGAAAGCGTCTGACCTTTCTCTGCAGGA 240
Db 8587 TAGGTCCCATTTGGAAAGCAAGTTCTGACCAAGTGGAAAGCGTCTGACCTTTCTCTGCAGGA 8646
QY 241 ACTTCTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db 8647 ACTTCTGTGTGGCTACAGCTGAAAGATGATGAACCTGAGCCGTGAGGCACCCATCGGTGG 8706
QY 301 CGACTTTCCAGCAGTTTCAGAAGCAGAAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 360
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QY 361 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db 8767 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTGAGAATATTTCTGACAGAGCA 8826
QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCACAGAGAGCTGCCCTCCTGAGGAGAG 480
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Db 9247 TTTGGAAGATCTGAATACACAGATGGAGGCTTCTACAGGTGGCTGTGGAGGACCGTGTGAG 9306
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Db 9307 ACAGCTGCATGAAGCCACACAGGACCTTTGGTCTCTGTCATCCAGCACITTCCTTTCCACTTC 9366
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Db 9367 AGTTGAGGTCCTCTGGGAGAGAGCCATCTCACCAAAACAAAGTGCCCTACTATATCAACCA 9426
QY 1021 CGAGACTCAACAACTTGTGGGACCATTCGCAAAATGACAGAGCTCTACCAAGTCTTTAGC 1080
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Db	9547	GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGACGTGCATGTGATGCCCTTGGACCCAGCA	9606
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Db	9667	AATTTATGATCGTCTGGAGCAAGAGCACAAATCTGGTCAATGTCCCTCTCTGTGTGGA	9726
Qy	1321	TATGTCTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT	1380
Db	9727	TATGTCTCTCAACTGGCTTCTCAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT	9786
Qy	1381	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTATAAGCACATTTGGAAGACAAGTACAG	1440
Db	9787	CCTGTCTTTTAAAACTGGCATCATTTCTCTGTGTAAAGCACACTTGGGAAGACAAGTACAG	9846
Qy	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT	1500
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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 07:39:06 ; Search time 408.027 Seconds
(without alignments)
15627.746 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1501	100.0	2169	6	AAD37232	Aad37232 Human dys
2	1501	100.0	3531	6	AAD37238	Aad37238 Human dys
3	1501	100.0	3858	6	AAD37237	Aad37237 Human dys
4	1501	100.0	3999	6	AAD37234	Aad37234 Human dys
5	1501	100.0	4182	6	AAD37230	Aad37230 Human dys
6	1501	100.0	4498	6	AAD37258	Aad37258 Adeno-ass
7	1501	100.0	4825	6	AAD37257	Aad37257 Adeno-ass
8	1501	100.0	4848	6	AAD37263	Aad37263 Adeno-ass
9	1501	100.0	4966	6	AAD37256	Aad37256 Adeno-ass
10	1501	100.0	4990	6	AAD37262	Aad37262 Adeno-ass
11	1501	100.0	5060	6	AAD37264	Aad37264 Adeno-ass
12	1501	100.0	5149	6	AAD37255	Aad37255 Adeno-ass
13	1501	100.0	5339	6	ABK81998	Abk81998 DNA encod
14	1501	100.0	5462	6	ABK81999	Abk81999 DNA encod
15	1501	100.0	5952	5	AAD06794	Aad06794 Human dys
16	1501	100.0	8689	6	ABK82000	Abk82000 DNA encod
17	1501	100.0	11058	6	AAD37229	Aad37229 Human dys
18	1501	100.0	11241	6	ABK82005	Abk82005 cDNA encod
19	1501	100.0	11443	6	ABK82002	Abk82002 DNA encod
20	1501	100.0	12923	1	AAN90338	Aan90338 Sequence
21	1501	100.0	13957	6	ABK81959	Abk81959 cDNA encod
22	1501	100.0	13957	6	ABT10904	Abt10904 Human bre
23	1501	100.0	13957	6	ABN95786	Abn95786 Gene #228

24	1501	100.0	13957	6	ABS69900	Abs69900 Human dys
25	1497.4	99.8	13977	6	ABS70403	Abs70403 Human bon
26	1307.8	87.1	3510	6	AAD37240	Aad37240 Human dys
27	1307.8	87.1	4476	6	AAD37259	Aad37259 Adeno-ass
28	1303	86.8	1821	6	AAD37241	Aad37241 Human dys
29	1298.4	86.5	13815	6	ABK81960	Abk81960 cDNA enco
30	1298.4	86.5	13815	6	ABI99799	Abi99799 Mouse isc
c 31	1298.4	86.5	19307	2	AAT27558	Aat27558 Shuttle v
32	1296.8	86.4	13815	2	AAV18885	Aav18885 Mus muscu
33	985.2	65.6	4402	3	AAZ48567	Aaz48567 A rod sho
34	917.6	61.1	3446	6	AAD37242	Aad37242 Human dys
35	917.6	61.1	4414	6	AAD37260	Aad37260 Adeno-ass
36	916.6	61.1	5417	6	ABK81997	Abk81997 DNA encod
37	916	61.0	1434	6	AAD37243	Aad37243 Human dys
38	786	52.4	4402	3	AAZ48568	Aaz48568 A rod sho
39	650.4	43.3	4075	3	AAZ48569	Aaz48569 A rod sho
40	646.2	43.1	3747	3	AAZ48566	Aaz48566 A rod sho
41	619.2	41.3	10705	7	ABT41896	Abt41896 Toxicity
42	619.2	41.3	11096	6	ABK81962	Abk81962 cDNA enco
43	604.8	40.3	6045	2	AAT74665	Aat74665 Utrophin
44	604.8	40.3	6059	4	AAF84673	Aaf84673 Nucleotid
45	604.8	40.3	9195	7	ACD19399	Acd19399 cDNA enco

ALIGNMENTS

RESULT 1	
AAD37232	
ID	AAD37232 standard; DNA; 2169 BP.
XX	
AC	AAD37232;
XX	
DT	21-AUG-2002 (first entry)
XX	
DE	Human dystrophin rod, hinge and CR domain regions encoding DNA #1.
XX	
KW	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW	adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW	Becker muscular dystrophy; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200183695-A2.
XX	
PD	08-NOV-2001.
XX	
PF	27-APR-2001; 2001WO-US013677.
XX	
PR	28-APR-2000; 2000US-0200777P.
XX	
PA	(XIAO/) XIAO X.
XX	
PI	Xiao X;
XX	
DR	WPI; 2002-049342/06.
XX	
PT	New dystrophin minigene for treating Duchenne or Becker muscular
PT	dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT	rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT	gene.
XX	
PS	Example 1; Page 45-46; 71pp; English.
XX	
CC	The present invention relates to an isolated nucleotide sequence encoding
CC	a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC	terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC	domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC	invention also relates to a recombinant adeno-associated virus (AAV)
CC	comprising dystrophin minigene operably linked to an expression control
CC	element. The dystrophin minigene in operable linkage with an expression
CC	control element, in a recombinant adeno-associated virus or retrovirus is
CC	useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular

CC	dystrophy (BMD) in a mammalian subject. The present sequence is human
CC	dystrophin DNA fragment encoding rods R22, R23 and R24, hinge H4 and CR
CC	domain regions
XX	
SQ	Sequence 2169 BP; 623 A; 529 C; 524 G; 493 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1501; DB 6; Length 2169;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	
QY	61 TGAACAACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTACA 120
Db	
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Db	
QY	271 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGAAAAAAGTCTCTCAACAT 330
Db	
QY	181 TAGGTCCCATTTGGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 240
Db	
QY	331 TAGGTCCCATTTGGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 390
Db	
QY	241 ACTTCTGGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db	
QY	391 ACTTCTGGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 450
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QY	301 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGGAATTGAA 360
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QY	451 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGGAATTGAA 510
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Db	
QY	511 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGCAGAGCA 570
Db	
QY	421 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 480
Db	
QY	571 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 630
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QY	481 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
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QY	631 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 690
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QY	541 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAATAAGATGAGACCCCTTGAAGACT 600
Db	
QY	691 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAATAAGATGAGACCCCTTGAAGACT 750
Db	
QY	601 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 660
Db	
QY	751 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 810
Db	
QY	661 CAAGGATCCTGGCAGCCCGTGGCGGATCTCCTCAATTGACTCTCTCCAAGATCACCTCGA 720
Db	
QY	811 CAAGGATCCTGGCAGCCCGTGGCGGATCTCCTCAATTGACTCTCTCCAAGATCACCTCGA 870
Db	
QY	721 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGTGAGCCACGTCAA 780
Db	
QY	871 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGTGAGCCACGTCAA 930
Db	
QY	781 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 840
Db	
QY	931 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 990
Db	
QY	841 TCTGGAAGACCTGAACACACAGATGAAGCTTCTGCAAGGTGGCGTTCGAGGACCGAGTCAG 900
Db	
QY	991 TCTGGAAGACCTGAACACACAGATGAAGCTTCTGCAAGGTGGCGTTCGAGGACCGAGTCAG 1050
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Db	
QY	1051 GCAGCTGCATGAAGCCCAAGGGACTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC 1110
Db	

QY	961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACCA 1020
Db	
QY	1111 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACCA 1170
Db	
QY	1021 CGAGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db	
QY	1171 CGAGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1230
Db	
QY	1081 TGACCTGAATAATGTCTAGATTCTCAGCTTATAGGACTGCCATGAAAATCCGAAGACTGCA 1140
Db	
QY	1231 TGACCTGAATAATGTCTAGATTCTCAGCTTATAGGACTGCCATGAAAATCCGAAGACTGCA 1290
Db	
QY	1141 GAAGGCCCTTGTCTGGATCTCTTGAAGCCTGTCTAGCTGCTGATGCTTGGACCAAGCA 1200
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QY	1291 GAAGGCCCTTGTCTGGATCTCTTGAAGCCTGTCTAGCTGCTGATGCTTGGACCAAGCA 1350
Db	
QY	1201 CAACCTCAAGCAAAATGACCCAGCCATGGATATCTCTGAGATTATTAATTGTTTGACCAC 1260
Db	
QY	1351 CAACCTCAAGCAAAATGACCCAGCCATGGATATCTCTGAGATTATTAATTGTTTGACCAC 1410
Db	
QY	1261 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGGA 1320
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QY	1411 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGGA 1470
Db	
QY	1321 TATGTGTCTGAATGCTGCTGAATGTTTATGATACGGGACCAACAGGAGGATCCGTGT 1380
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QY	1471 TATGTGTCTGAATGCTGCTGAATGTTTATGATACGGGACCAACAGGAGGATCCGTGT 1530
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QY	1381 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAAGTACAG 1440
Db	
QY	1531 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAAGTACAG 1590
Db	
QY	1441 ATACCTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGGCTGGGCTT 1500
Db	
QY	1591 ATACCTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGGCTGGGCTT 1650
Db	
QY	1501 C 1501
Db	1651 C 1651

RESULT 2	
AAD37238	
ID	AAD37238 standard; DNA; 3531 BP.
XX	
AC	AAD37238;
XX	
DT	21-AUG-2002 (first entry)
XX	
DE	Human dystrophin minigene delta3531.
XX	
KW	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW	adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
XX	Becker muscular dystrophy; ds.
OS	Homo sapiens.
XX	
PN	WO200183695-A2.
XX	
PD	08-NOV-2001.
XX	
PF	27-APR-2001; 2001WO-US013677.
XX	
PR	28-APR-2000; 2000US-0200777P.
XX	
PA	(XIAO/) XIAO X.
XX	
PI	Xiao X;
XX	
DR	WPI; 2002-049342/06.
XX	
PT	New dystrophin minigene for treating Duchenne or Becker muscular

PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.

Example 1; Page 50-51; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene Delta3531 containing nucleotides 1-1341 (N-terminus, hinge H1 and rod R1), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids)

XX WO200183695-A2.
PN
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX
PT New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 48-49; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta3849 containing nucleotides 1-1668 (N-terminus,
CC hinge H1 and rods R1, R2), 8059-10227 (rods R22, R23 and R24, hinge H4
CC and CR domain) and 11047-11058 (dystrophin last 3 amino acids)
XX
SQ Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 U; 0 Other;
Query Match 100.0%; Score 1501; DB 6; Length 3858;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAAGGTGAAATTTGAAGCTCACACAGATGTTTATCAACAACCTGGA 60
Db 1827 ACAATGGCAAGACCTCCAAAGGTGAAATTTGAAGCTCACACAGATGTTTATCAACAACCTGGA 1886
QY 61 TGAACAACAGCCAAAAATCCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACA 120
Db 1887 TGAACAACAGCCAAAAATCCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACA 1945
QY 121 AAGACGTTTGGATAACATGAATCAAGTGGAGTGAATTCGGAAGAAAGTCTCTCAACAT 180
Db 1947 AAGACGTTTGGATAACATGAATCAAGTGGAGTGAATTCGGAAGAAAGTCTCTCAACAT 2005
QY 181 TAGTCCCATTTTGGAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 2007 TAGTCCCATTTTGGAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 2066
QY 241 ACTTCTGGTGTGGCTACAGTGAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG 300
Db 2067 ACTTCTGGTGTGGCTACAGTGAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG 2126
QY 301 CGACTTTCCAGCAGTTTCAGAACGAGAACGATGTACATAGGGCCCTTCAGAGGGAAATTGAA 360
Db 2127 CGACTTTCCAGCAGTTTCAGAACGAGAACGATGTACATAGGGCCCTTCAGAGGGAAATTGAA 2186
QY 361 AACTAAGAACCTGTATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db 2187 AACTAAGAACCTGTATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA 2246
QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACAGAGGCCCCAGAGAGCTGCTCCTGAGGAGAG 480
Db 2247 GCCTTTGGAAGGACTAGAGAAACTCTACAGAGGCCCCAGAGAGCTGCTCCTGAGGAGAG 2306

QY 481 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db 2307 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 2366
QY 541 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 600
Db 2367 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 2426
QY 601 CCAGGAACCTCAAGAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 660
Db 2427 CCAGGAACCTCAAGAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 2486
QY 661 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
Db 2487 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 2546
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAACTGAGCCACGTCAA 780
Db 2547 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAACTGAGCCACGTCAA 2606
QY 781 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTTGAGCTCTCACCGTATTAACCTCAGCAC 840
Db 2607 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTTGAGCTCTCACCGTATTAACCTCAGCAC 2666
QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGACAGTGGCCGCTCGAGGACCGAGTCAG 900
Db 2667 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGACAGTGGCCGCTCGAGGACCGAGTCAG 2726
QY 901 GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGATCTCAGCACTTCTTTCCACGTC 960
Db 2727 GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGATCTCAGCACTTCTTTCCACGTC 2786
QY 961 TGTCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020
Db 2787 TGTCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 2846
QY 1021 CGAGACTCAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGC 1080
Db 2847 CGAGACTCAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGC 2906
QY 1081 TGACCTGAATAATGTCAGATTTCAAGTTTATAGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 2907 TGACCTGAATAATGTCAGATTTCAAGTTTATAGACTGCCATGAAACTCCGAAGACTGCA 2966
QY 1141 GAAGGCCCTTTGCTTGGATCTTTGAGCCCTGTCAGCTGCATGTGATGCTTGGACCCAGCA 1200
Db 2967 GAAGGCCCTTTGCTTGGATCTTTGAGCCCTGTCAGCTGCATGTGATGCTTGGACCCAGCA 3026
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGTCAGATTATTAATTGTTGACCCAC 1260
Db 3027 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGTCAGATTATTAATTGTTGACCCAC 3086
QY 1261 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
Db 3087 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 3146
QY 1321 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1380
Db 3147 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 3206
QY 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAG 1440
Db 3207 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAG 3266
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGCCT 1500
Db 3267 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGCCT 3326
QY 1501 C 1501
Db 3327 C 3327

RESULT 4
AAD37234
ID AAD37234 standard; DNA; 3999 BP.
XX
AC AAD37234;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human dystrophin minigene delta3990.
XX
DE Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
XX 27-APR-2001; 2001WO-US013677.
PF
XX 28-APR-2000; 2000US-0200777P.
PR
XX (XIAO/) XIAO X.
PA
XX Xiao X;
PI
XX
DR WPI; 2002-049342/06.
XX
XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 46-47; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta3990 containing nucleotides 1-1668 (N-terminus,
CC hinge H1 and rods R1 and R2), 8059-10227 (rods R22, R23 and R24, hinge H4
CC and CR domain) and 11047-11058 (dystrophin last 3 amino acids)
XX
SQ Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 U; 0 Other;

Query Match 100.0%; Score 1501; DB 6; Length 3999;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACTGGA 60
Db
QY 61 TGAAAACAGCCAAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCGAGTCCTGTTACA 120
Db 2028 TGAAAACAGCCAAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCGAGTCCTGTTACA 2087

QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 180
Db 2088 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 2147

QY 181 TAGGTCCCATTTGGAGCCAGATTCTGACCCAGTGAAGCGTCTGACCTTTCTCTGCAGGA 240
Db 2148 TAGGTCCCATTTGGAGCCAGATTCTGACCCAGTGAAGCGTCTGACCTTTCTCTGCAGGA 2207

QY 241 ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db
QY 301 CGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGGAATTGAA 360
Db
QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db
QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCACAGAGAGCTGCCTCCTGAGGAGAG 480
Db
QY 481 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db
QY 541 AAAATTGAACCTCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 600
Db
QY 601 CCAGGAACTTCAAGAGGCCACGGATGAGCTGAGCCTCAAGCTGGCCCAAGCTGAGGTGAT 660
Db
QY 661 CAAGGGATCCTGGAGCCCGTGGCGGATCTCTCATTTGAGCTCTCAAGATCACCTCGA 720
Db
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAAAATTGGCCCTCTGAAAGAGAACGTGAGCCACGTCAA 780
Db
QY 781 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAAGCCTCAGCAC 840
Db
QY 841 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG 900
Db
QY 901 GCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC 960
Db
QY 961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCCAACAAAGTGCCCTACTATATCAACCA 1020
Db
QY 1021 CGAGACTCAAACAACTTCTGTTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db
QY 1081 TGACCTGAATAATGTCAATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
Db
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACACGCA 1200
Db
QY 1201 CAACTCAAGCAAAAATGACAGCCCATGGATATCCTGCAGATTATTAAATTGTTGACCCAC 1260
Db
QY 1261 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1320
Db
QY 1320 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1380
Db
QY 1380 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1440
Db
QY 1440 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1500
Db
QY 1500 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1560
Db
QY 1560 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1620
Db
QY 1620 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1680
Db
QY 1680 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1740
Db
QY 1740 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1800
Db
QY 1800 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1860
Db
QY 1860 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1920
Db
QY 1920 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 1980
Db
QY 1980 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2040
Db
QY 2040 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2100
Db
QY 2100 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2160
Db
QY 2160 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2220
Db
QY 2220 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2280
Db
QY 2280 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2340
Db
QY 2340 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2400
Db
QY 2400 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2460
Db
QY 2460 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2520
Db
QY 2520 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2580
Db
QY 2580 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2640
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QY 2640 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2700
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QY 2700 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2760
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QY 2760 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2820
Db
QY 2820 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2880
Db
QY 2880 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 2940
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QY 2940 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3000
Db
QY 3000 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3060
Db
QY 3060 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3120
Db
QY 3120 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3180
Db
QY 3180 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3240
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QY 3240 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3300
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QY 3300 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3360
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QY 3360 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3420
Db
QY 3420 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3480
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QY 3480 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3540
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QY 3780 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3840
Db
QY 3840 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3900
Db
QY 3900 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 3960
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QY 3960 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4020
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Db
QY 4080 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4140
Db
QY 4140 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4200
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QY 4200 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4260
Db
QY 4260 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4320
Db
QY 4320 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4380
Db
QY 4380 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4440
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QY 4440 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4500
Db
QY 4500 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4560
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QY 4560 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4620
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QY 4620 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4680
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QY 4680 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4740
Db
QY 4740 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4800
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QY 4800 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4860
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QY 4860 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4920
Db
QY 4920 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 4980
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QY 4980 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5040
Db
QY 5040 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5100
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QY 5100 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5160
Db
QY 5160 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5220
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QY 5280 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5340
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QY 5340 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5400
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QY 5400 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5460
Db
QY 5460 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5520
Db
QY 5520 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5580
Db
QY 5580 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5640
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QY 5640 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5700
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QY 5700 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5760
Db
QY 5760 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5820
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QY 5820 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5880
Db
QY 5880 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 5940
Db
QY 5940 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6000
Db
QY 6000 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6060
Db
QY 6060 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6120
Db
QY 6120 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6180
Db
QY 6180 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6240
Db
QY 6240 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6300
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QY 6300 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6360
Db
QY 6360 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6420
Db
QY 6420 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6480
Db
QY 6480 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6540
Db
QY 6540 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6600
Db
QY 6600 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6660
Db
QY 6660 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6720
Db
QY 6720 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6780
Db
QY 6780 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6840
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QY 6840 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6900
Db
QY 6900 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 6960
Db
QY 6960 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7020
Db
QY 7020 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7080
Db
QY 7080 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7140
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QY 7140 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7200
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QY 7200 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7260
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QY 7260 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7320
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QY 7320 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7380
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QY 7380 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 7440
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QY 8280 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 8340
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QY 9000 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 9060
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QY 9060 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 9120
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QY 9120 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 9180
Db
QY 9180 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 9240
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QY 9240 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 9300
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Db
QY 9780 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 9840
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QY 9960 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 10020
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QY 13500 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 13560
Db
QY 13560 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCTCTCTGCGTGA 13620
Db
QY 13620 TATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGT

QY 1081 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
DB 3231 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 3290
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCCTGGACGCA 1200
DB 3291 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCCTGGACGCA 3350
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCCAC 1260
DB 3351 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCCAC 3410
QY 1261 TATTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGA 1320
DB 3411 TATTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGA 3470
QY 1321 TATGTCTCTGAACCTGGCTGCTGAATGTTTATGATACGGAGCAACAGGGAGGATCCGTGT 1380
DB 3471 TATGTCTCTGAACCTGGCTGCTGAATGTTTATGATACGGAGCAACAGGGAGGATCCGTGT 3530
QY 1381 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1440
DB 3531 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 3590
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTGGCAAGTTCACAGGATTTTGTGACCGCAGCGCTGGGCCT 1500
DB 3591 ATACCTTTTCAAGCAAGTGGCAAGTTCACAGGATTTTGTGACCGCAGCGCTGGGCCT 3650
QY 1501 C 1501
DB 3651 C 3651

RESULT 6
AAD37258
ID AAD37258 standard; DNA; 4498 BP.
XX
AC AAD37258;
XX
DT 21-AUG-2002 (first entry)
XX
DE Adeno-associated virus vector plasmid, AAV-MCK-3531.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX
PT New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 62-63; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding

CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence
XX
SQ Sequence 4498 BP; 1251 A; 1118 C; 1123 G; 1006 T; 0 U; 0 Other;

Query Match 100.0%; Score 1501; DB 6; Length 4498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAAGGTGAATTTGAAGCTCACACAGATGTTTATCACAACTGGA 60
DB 2257 ACAATGGCAAGACCTCCAAAGGTGAATTTGAAGCTCACACAGATGTTTATCACAACTGGA 2316
QY 61 TGAAAACAGCAAAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCTCTTTACA 120
DB 2317 TGAAAACAGCAAAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCTCTTTACA 2376
QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGAAAAAAGTCTCTCAACAT 180
DB 2377 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGAAAAAAGTCTCTCAACAT 2436
QY 181 TAGGTCCCATTTGGAAGCCAGTTCTGACCCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 240
DB 2437 TAGGTCCCATTTGGAAGCCAGTTCTGACCCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 2496
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
DB 2497 ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 2556
QY 301 CGACTTTCAGCAGTTTCAAGAGCAGACCATGTACATAGGGCCCTTCAAGAGGGGAATTGAA 360
DB 2557 CGACTTTCAGCAGTTTCAAGAGCAGACCATGTACATAGGGCCCTTCAAGAGGGGAATTGAA 2616
QY 361 AACTAAAGAACCTGTAAATCATGACTACTTGTGAGACTGTACGAATATTTCTGACAGAGCA 420
DB 2617 AACTAAAGAACCTGTAAATCATGACTACTTGTGAGACTGTACGAATATTTCTGACAGAGCA 2676
QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACAGAGGCCCCAGAGAGCTGCCTCCTGAGGAGAG 480
DB 2677 GCCTTTGGAAGGACTAGAGAAACTCTACAGAGGCCCCAGAGAGCTGCCTCCTGAGGAGAG 2736
QY 481 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
DB 2737 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 2796
QY 541 AAAATTGAACCTTGCACTCCGCTGACTGGCAGAGAAAAAATAGATGAGACCTTTGAAAGACT 600
DB 2797 AAAATTGAACCTTGCACTCCGCTGACTGGCAGAGAAAAAATAGATGAGACCTTTGAAAGACT 2856
QY 601 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGAT 660
DB 2857 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGAT 2916
QY 661 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
DB 2917 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 2976
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGCTGAGCCACGTCAA 780
DB 2977 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGCTGAGCCACGTCAA 3036
QY 781 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 840
DB 3037 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 3096

QY 841 TCTGGAAGACCTGAACACACAGATGGAGCTTCTGCAGGTGGCGTCGAGGACCGAGTCAG 900
Db TCTGGAAGACCTGAACACACAGATGGAGCTTCTGCAGGTGGCGTCGAGGACCGAGTCAG 3156
QY 901 GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 960
Db GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 3216
QY 961 TGTCCAGGTCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020
Db TGTCCAGGTCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 3276
QY 1021 CGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db CGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 3336
QY 1081 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACCTCCGAAGACTGCA 1140
Db TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACCTCCGAAGACTGCA 3396
QY 1141 GAAGGCCCTTTGCTTGGATCTCTGAGCCTGTGAGCTGCATGTGATGCCTTGACACGCA 1200
Db GAAGGCCCTTTGCTTGGATCTCTGAGCCTGTGAGCTGCATGTGATGCCTTGACACGCA 3456
QY 1201 CAACCTCAAGCAAAATGACAGCCATGGATATCCTGAGATTATTAATTGTTGACCCAC 1260
Db CAACCTCAAGCAAAATGACAGCCATGGATATCCTGAGATTATTAATTGTTGACCCAC 3516
QY 1261 TATTATGACCGCCTGGAGAGAGCAACAATTTGGTCAACGTCCTCTCTCGGTGGA 1320
Db TATTATGACCGCCTGGAGAGAGCAACAATTTGGTCAACGTCCTCTCTCGGTGGA 3576
QY 1321 TATGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380
Db TATGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 3636
QY 1381 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAG 1440
Db CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAG 3696
QY 1441 ATACTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCGCAGGCTGGGCCT 1500
Db ATACTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCGCAGGCTGGGCCT 3756
QY 1501 C 1501
Db 3757 C 3757

RESULT 7
AAD37257
ID AAD37257 standard; DNA; 4825 BP.
XX
AC AAD37257;
XX
DT 21-AUG-2002 (first entry)
XX
DE Adeno-associated virus vector plasmid, AAV-MCK-delta3849.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.

XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX
PT New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 61-62; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence
XX
SQ Sequence 4825 BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 U; 0 Other;

Query Match 100.0%; Score 1501; DB 6; Length 4825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCAAGGTGAAATTGAAGCTCACACAGATGTTTATCAACACCTGGA 60
Db 2584 ACAATGGCAAGACCTCAAGGTGAAATTGAAGCTCACACAGATGTTTATCAACACCTGGA 2643
QY 61 TGAAAACAGCCAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGAGTCCCTGTTACA 120
Db 2644 TGAAAACAGCCAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGAGTCCCTGTTACA 2703
QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAGTCTCTCAACAT 180
Db 2704 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAGTCTCTCAACAT 2763
QY 181 TAGGTCCCATTTGGAAGCCAGTTCTGACCCAGTGAAGCGTCTGACCTTTCTCTGCAGGA 240
Db 2764 TAGGTCCCATTTGGAAGCCAGTTCTGACCCAGTGAAGCGTCTGACCTTTCTCTGCAGGA 2823
QY 241 ACTTCTGGTGTGGTACAGCTGAAAGATGATGAATTAAGCCGCGCAGGACCTATTGGAGG 300
Db 2824 ACTTCTGGTGTGGTACAGCTGAAAGATGATGAATTAAGCCGCGCAGGACCTATTGGAGG 2883
QY 301 CGACTTTCCAGCAGTTCAAGAGCAGAACCGATGTACATAGGGCCTTCAAGAGGGGAATTGAA 360
Db 2884 CGACTTTCCAGCAGTTCAAGAGCAGAACCGATGTACATAGGGCCTTCAAGAGGGGAATTGAA 2943
QY 361 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db 2944 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 3003
QY 421 GCCTTTTGGAAAGGACTAGAGAACTCTACAGGAGCCCGAGAGGCTCCCTCTGAGGAGAG 480
Db 3004 GCCTTTTGGAAAGGACTAGAGAACTCTACAGGAGCCCGAGAGGCTCCCTCTGAGGAGAG 3063
QY 481 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db 3064 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 3123
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTTGAAAGACT 600

Db	3124	AAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT	3183	DT	21-AUG-2002	(first entry)
Qy	601	CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCCAAGCTGAGGTGAT	660	XX	Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849.	
Db	3184	CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCCAAGCTGAGGTGAT	3243	XX		
Qy	661	CAAGGATCCTGGCAGCCCGTGGCGGATCTCCTCATGTACTCTCTCCAAGATCACCTCGA	720	KW	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;	
Db	3244	CAAGGATCCTGGCAGCCCGTGGCGGATCTCCTCATGTACTCTCTCCAAGATCACCTCGA	3303	KW	adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;	
Qy	721	GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGTGAGCCACGTCAA	780	XX	Becker muscular dystrophy; ds.	
Db	3304	GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGTGAGCCACGTCAA	3363	OS	Homo sapiens.	
Qy	781	TGACCTTGCTCGCCAGCTTACCAGCTTTGGCATTTCAGCTCTCACCGTATAACCTCAGCAC	840	OS	Cytomegalovirus.	
Db	3364	TGACCTTGCTCGCCAGCTTACCAGCTTTGGCATTTCAGCTCTCACCGTATAACCTCAGCAC	3423	OS	Unidentified.	
Qy	841	TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGTGGCCGTCGAGGACCGAGTCAG	900	OS	Chimeric.	
Db	3424	TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGTGGCCGTCGAGGACCGAGTCAG	3483	XX		
Qy	901	GCAGCTGCATGAAGCCCAACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC	960	PN	WO200183695-A2.	
Db	3484	GCAGCTGCATGAAGCCCAACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC	3543	XX	08-NOV-2001.	
Qy	961	TGTCCAGGTCCTGGGAGAGAGCCATCTGCCAAACAAAGTGCCCTACTATATCAACCA	1020	XX	27-APR-2001; 2001WO-US013677.	
Db	3544	TGTCCAGGTCCTGGGAGAGAGCCATCTGCCAAACAAAGTGCCCTACTATATCAACCA	3603	PR	28-APR-2000; 2000US-0200777P.	
Qy	1021	CGAGACTCAAAACAACTTGCTGGGACCATCCAAATGACAGAGCTCTACCACTCTTTAGC	1080	XX	(XIAO/) XIAO X.	
Db	3604	CGAGACTCAAAACAACTTGCTGGGACCATCCAAATGACAGAGCTCTACCACTCTTTAGC	3663	PI	Xiao X;	
Qy	1081	TGACCTGATTAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA	1140	XX	WPI; 2002-049342/06.	
Db	3664	TGACCTGATTAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA	3723	XX	New dystrophin minigene for treating Duchenne or Becker muscular	
Qy	1141	GAAGGCCCTTTGCTTGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA	1200	PT	dystrophy comprises an N-terminal domain or modified N-terminal domain,	
Db	3724	GAAGGCCCTTTGCTTGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA	3783	PT	rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin	
Qy	1201	CAACCTCAAGCAAAATGACCGCCATGGATATCCTGCAGATTATTAATTGTTGACCA	1260	PT	gene.	
Db	3784	CAACCTCAAGCAAAATGACCGCCATGGATATCCTGCAGATTATTAATTGTTGACCA	3843	XX	Example 1; Page 68-70; 71pp; English.	
Qy	1261	TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA	1320	XX	The present invention relates to an isolated nucleotide sequence encoding	
Db	3844	TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA	3903	CC	a dystrophin minigene. The minigene comprises N-terminal or modified N-	
Qy	1321	TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGACAGGGAGGATCCGTGT	1380	CC	terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4	
Db	3904	TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGACAGGGAGGATCCGTGT	3963	CC	domains and cysteine-rich domains of dystrophin or utrophin genes. The	
Qy	1381	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	1440	CC	invention also relates to a recombinant adeno-associated virus (AAV)	
Db	3964	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	4023	CC	comprising dystrophin minigene operably linked to an expression control	
Qy	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGGCCT	1500	CC	element. The dystrophin minigene in operable linkage with an expression	
Db	4024	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGGCCT	1500	CC	control element, in a recombinant adeno-associated virus or retrovirus is	
Qy	1501	C 1501	1501	CC	useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular	
Db	4084	C 4084	4084	CC	dystrophy (BMD) in a mammalian subject. The present sequence is AAV	
RESULT 8				CC	vector plasmid construct containing human dystrophin minigenes, a	
AAD37263				CC	cytomegalovirus (CMV) promoter and a small polyA signal sequence	
ID	AAD37263	standard; DNA; 4848 BP.		XX	Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 U; 0 Other;	
XX				XX	Query Match 100.0%; Score 1501; DB 6; Length 4848;	
AC	AAD37263;			XX	Best Local Similarity 100.0%; Pred. NO. 0;	
XX				XX	Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY 301 CGACTTTCCAGCAGTTTCAAGACGAGATGTACATAGGGCTTCAAGAGGGAATTGAA 360
Db 2907 CGACTTTCCAGCAGTTTCAAGACGAGATGTACATAGGGCTTCAAGAGGGAATTGAA 2966
QY 361 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCA 420
Db 2967 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCA 3026
QY 421 GCCTTTGGAAGACTAGAGAACTCTACAGAGGAGCCCGAGAGAGCTGCCTCCTGAGGAGAG 480
Db 3027 GCCTTTGGAAGACTAGAGAACTCTACAGAGGAGCCCGAGAGAGCTGCCTCCTGAGGAGAG 3086
QY 481 AGCCAGAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db 3087 AGCCAGAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 3146
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAGAAATAGATGAGACCCCTTGAAAGACT 600
Db 3147 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAGAAATAGATGAGACCCCTTGAAAGACT 3206
QY 601 CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 660
Db 3207 CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 3266
QY 661 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGAGTCTCTCCAAGATCACCTCGA 720
Db 3267 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGAGTCTCTCCAAGATCACCTCGA 3326
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGCTGAGCCACGTCAA 780
Db 3327 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGCTGAGCCACGTCAA 3386
QY 781 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 840
Db 3387 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 3446
QY 841 TCTGGAAGACCTGAACACCAAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAG 900
Db 3447 TCTGGAAGACCTGAACACCAAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAG 3506
QY 901 GCAGTGCATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC 960
Db 3507 GCAGTGCATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC 3566
QY 961 TGTCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACCA 1020
Db 3567 TGTCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACCA 3626
QY 1021 CGAGACTCAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGC 1080
Db 3627 CGAGACTCAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGC 3686
QY 1081 TGACCTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 3687 TGACCTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 3746
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTCAGCTGCATGTGATGCTTGGACCAGCA 1200
Db 3747 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTCAGCTGCATGTGATGCTTGGACCAGCA 3806
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCTCTGCAGATTATTAATTGTTGACCCAC 1260
Db 3807 CAACCTCAAGCAAAATGACAGCCCATGGATATCTCTGCAGATTATTAATTGTTGACCCAC 3866
QY 1261 TATTTATGACCGCTTGAGCAAGAGCACAATAATTTGGTCAACGTCCTCTCTGCGTGGA 1320
Db 3867 TATTTATGACCGCTTGAGCAAGAGCACAATAATTTGGTCAACGTCCTCTCTGCGTGGA 3926
QY 1321 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGACAGGGAGGATCCGCTGT 1380
Db 3927 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGACAGGGAGGATCCGCTGT 3986
QY 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAAGTACAG 1440

Db 3987 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 4046
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGSCCT 1500
Db 4047 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGSCCT 4106
QY 1501 C 1501
Db 4107 C 4107
RESULT 9
AAD37256
ID AAD37256 standard; DNA; 4966 BP.
XX AAD37256;
AC AAD37256;
XX 21-AUG-2002 (first entry)
XX Adeno-associated virus vector plasmid, AAV-MCK-delta3990.
DE Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
XX adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX Homo sapiens.
OS Unidentified.
OS Chimeric.
XX WO200183695-A2.
PN 08-NOV-2001.
PD 27-APR-2001; 2001WO-US013677.
XX 28-APR-2000; 2000US-0200777P.
PR (XIAO/) XIAO X.
XX XIAO X;
PI WPI; 2002-049342/06.
XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX Example 1; Page 59-60; 71pp; English.
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene operably linked to an expression control
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence
XX Sequence 4966 BP; 1403 A; 1216 C; 1232 G; 1115 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 1501; DB 6; Length 4966;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCCAAGGTGAATGAAGCTCACACAGATGTTTATCACAACCTGGA 60
Db 2725 ACAATGGCAAGACCTCCCAAGGTGAATGAAGCTCACACAGATGTTTATCACAACCTGGA 2784

QY	61	TGAAACAGCCAAATACTCTGAGATCCCTGGAGGTTCCGATGATGACACTCCTGTTACA	120	QY	1141	GAAGCCCTTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATCCCTTGACACGCA	1200
Db	2785	TGAAACAGCCAAATACTCTGAGATCCCTGGAGGTTCCGATGATGACACTCCTGTTACA	2844	Db	3865	GAAGCCCTTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATCCCTTGACACGCA	3924
QY	121	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACAT	180	QY	1201	CAACCTCAAGCAAAATGACACGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC	1260
Db	2845	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACAT	2904	Db	3925	CAACCTCAAGCAAAATGACACGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC	3984
QY	181	TAGTCCCATTTGGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGA	240	QY	1261	TATTTATGACCGCCTGGAGCAAGACACAACAATTTGGTCAACGTCCCTCTCTGCGTGA	1320
Db	2905	TAGTCCCATTTGGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGA	2964	Db	3985	TATTTATGACCGCCTGGAGCAAGACACAACAATTTGGTCAACGTCCCTCTCTGCGTGA	4044
QY	241	ACTTCTGGTGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG	300	QY	1321	TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT	1380
Db	2965	ACTTCTGGTGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG	3024	Db	4045	TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT	4104
QY	301	CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA	360	QY	1381	CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	1440
Db	3025	CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA	3084	Db	4105	CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	4164
QY	361	AACATAAGAACCTGTAAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGCAGAGCA	420	QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCT	1500
Db	3085	AACATAAGAACCTGTAAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGCAGAGCA	3144	Db	4165	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCT	4224
QY	421	GCCTTTTGAAGGACTAGAGAACTCTACCAAGGAGCCAGAGCTGCCTCCTGAGAGAG	480	QY	1501	C 1501	
Db	3145	GCCTTTTGAAGGACTAGAGAACTCTACCAAGGAGCCAGAGCTGCCTCCTGAGAGAG	3204	Db	4225	C 4225	
QY	481	AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATACTAGTGGGA	540	RESULT 10			
Db	3205	AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATACTAGTGGGA	3264	AAD37262			
QY	541	AAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT	600	ID AAD37262 standard; DNA; 4990 BP.			
Db	3265	AAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT	3324	XX	AAD37262;		
QY	601	CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT	660	XX	21-AUG-2002 (first entry)		
Db	3325	CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT	3384	DE	Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3990.		
QY	661	CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA	720	XX	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;		
Db	3385	CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA	3444	KW	adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;		
QY	721	GAAAGTCAAGGCACTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGCTGAGCCACGTCAA	780	KW	Becker muscular dystrophy; ds.		
Db	3445	GAAAGTCAAGGCACTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGCTGAGCCACGTCAA	3504	XX	Homo sapiens.		
QY	781	TGACCTTGCTCGCCAGCTTACCACCTTTGGGATTCAGCTCTCACCGTATACCTCAGCAC	840	OS	Cytomegalovirus.		
Db	3505	TGACCTTGCTCGCCAGCTTACCACCTTTGGGATTCAGCTCTCACCGTATACCTCAGCAC	3564	OS	Unidentified.		
QY	841	TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG	900	OS	Chimeric.		
Db	3565	TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG	3624	XX	WO200183695-A2.		
QY	901	GCAGCTGCATGAAGCCCAAGGGACTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC	960	PN	08-NOV-2001.		
Db	3625	GCAGCTGCATGAAGCCCAAGGGACTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC	3684	PD	27-APR-2001; 2001WO-US013677.		
QY	961	TGTCCAGGGTCCCTGGGAGAGGCCATCTCGCCCAACAAAGTGCCCTACTATATCAACCA	1020	PD	28-APR-2000; 2000US-0200777P.		
Db	3685	TGTCCAGGGTCCCTGGGAGAGGCCATCTCGCCCAACAAAGTGCCCTACTATATCAACCA	3744	XX	(XIAO/) XIAO X.		
QY	1021	CGAGACTCAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGC	1080	XX	Xiao X;		
Db	3745	CGAGACTCAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGC	3804	PI	WPI; 2002-049342/06.		
QY	1081	TGACTGAAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA	1140	DR	New dystrophin minigene for treating Duchenne or Becker muscular		
Db	3805	TGACTGAAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA	3864	PT	dystrophy comprises an N-terminal domain or modified N-terminal domain,		
				PT	rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin		
				PT	gene.		
				XX	Example 1; Page 67-68; 71pp; English.		
				XX	The present invention relates to an isolated nucleotide sequence encoding		
				CC	a dystrophin minigene. The minigene comprises N-terminal or modified N-		
				CC	terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4		
				CC	domains and cysteine-rich domains of dystrophin or utrophin genes. The		

CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a
CC cytomegalovirus (CMV) promoter and a small polyA signal sequence
XX
SQ Sequence 4990 BP; 1439 A; 1185 C; 1208 G; 1158 T; 0 U; 0 Other;

Query Match 100.0%; Score 1501; DB 6; Length 4990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAAGGTGAATTTGAAGCTCACACAGATGTTTATCACAACCTGGA 60
DB 2749 ACAATGGCAAGACCTCCAAAGGTGAATTTGAAGCTCACACAGATGTTTATCACAACCTGGA 2808
QY 61 TGAACAACAGCCAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 120
DB 2809 TGAACAACAGCCAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 2868
QY 121 AAGACGTTTGGATAAATGAACTTCAAGTGGAGTGAACCTTCGGAATAAGTCTCTCAACAT 180
DB 2869 AAGACGTTTGGATAAATGAACTTCAAGTGGAGTGAACCTTCGGAATAAGTCTCTCAACAT 2928
QY 181 TAGGTCCCAATTTGGAAGCCAGTTCTGACAGTGGAAGCGTCTGCACCTTTCTCTGCAGGA 240
DB 2929 TAGGTCCCAATTTGGAAGCCAGTTCTGACAGTGGAAGCGTCTGCACCTTTCTCTGCAGGA 2988
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
DB 2989 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 3048
QY 301 CGACTTTCAGCAGTTTCAGAAAGCAGACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 360
DB 3049 CGACTTTCAGCAGTTTCAGAAAGCAGACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 3108
QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
DB 3109 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 3168
QY 421 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGGCCAGAGAGCTGCCTCTGAGGAGAG 480
DB 3169 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGGCCAGAGAGCTGCCTCTGAGGAGAG 3228
QY 481 AGCCAGAAATGTCACTCGGTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGA 540
DB 3229 AGCCAGAAATGTCACTCGGTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGA 3288
QY 541 AAAATTGAACCTGCACCTCGCTGACTGGCAGAGAAATAAGATGAGACCTTGAAGACT 600
DB 3289 AAAATTGAACCTGCACCTCGCTGACTGGCAGAGAAATAAGATGAGACCTTGAAGACT 3348
QY 601 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 660
DB 3349 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 3408
QY 661 CAAGGGATCTCTGGAGCCCGTGGCGATCTCCTCATTGACTCTCTCAAGATCACCTCGA 720
DB 3409 CAAGGGATCTCTGGAGCCCGTGGCGATCTCCTCATTGACTCTCTCAAGATCACCTCGA 3468
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCTCTTGAAGAGAGACGTGAGCCACGTCAA 780
DB 3469 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCTCTTGAAGAGAGACGTGAGCCACGTCAA 3528
QY 781 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 840
DB 3529 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 3588
QY 841 TCTGGAAGACCTGAAACACACAGATGGAAGCTTCTGAGGTGGCGCTGAGGACCGAGTCA 900

DB 3589 TCTGGAAGACCTTGAACACACAGATGGAAGCTTCTGAGGTGGCGCTCGAGGACCGAGTCAG 3648
QY 901 GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGACATTTCTTCCACGTC 960
DB 3649 GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGACATTTCTTCCACGTC 3708
QY 961 TGTCCAGGGTCCCTGGGAGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCA 1020
DB 3709 TGTCCAGGGTCCCTGGGAGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCA 3768
QY 1021 CGAGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
DB 3769 CGAGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 3828
QY 1081 TGACCTGAATAATGTGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
DB 3829 TGACCTGAATAATGTGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 3888
QY 1141 GAAGGCCCTTGTGGATCTCTGAGCCTGTGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 3889 GAAGGCCCTTGTGGATCTCTGAGCCTGTGATGATGATGATGATGATGATGATGATGATGAT 3948
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACAC 1260
DB 3949 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACAC 4008
QY 1261 TATTTATGACCGCCTGGAGCAAGAGACACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
DB 4009 TATTTATGACCGCCTGGAGCAAGAGACACAATTTGGTCAACGTCCTCTCTGCGTGA 4068
QY 1321 TATGCTGTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380
DB 4069 TATGCTGTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 4128
QY 1381 CCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGACACATTGGAAGACAAAGTACAG 1440
DB 4129 CCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGACACATTGGAAGACAAAGTACAG 4188
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCGGAGGCTGGGCT 1500
DB 4189 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCGGAGGCTGGGCT 4248
QY 1501 C 1501
DB 4249 C 4249

RESULT 11
AAD37264

ID AAD37264 standard; DNA; 5060 BP.

XX AAD37264;

XX 21-AUG-2002 (first entry)

XX Adeno-associated virus (AAV) vector plasmid, AAV-E-CMV-3849.

XX Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
XX adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
XX Becker muscular dystrophy; ds.

OS Homo sapiens.
OS Cytomegalovirus.
OS Unidentified.
OS Chimeric.

XX WO200183695-A2.

PN 08-NOV-2001.

XX 27-APR-2001; 2001WO-US013677.

XX 28-APR-2000; 2000US-0200777P.

XX (XIAO/) XIAO X.
XX PA
XX XX
PI xiao X;
XX WPI; 2002-049342/06.
XX
XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 70-71; 7lpp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) enhancer, a cytomegalovirus (CMV) promoter and a
CC small polyA signal sequence
XX
SQ Sequence 5060 BP; 1449 A; 1217 C; 1234 G; 1160 T; 0 U; 0 Other;
Query Match 100.0%; Score 1501; DB 6; Length 5060;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAGGTGAATGAAGCTCACACAGATGTTTATCAACAACCTGGA 50
Db
QY 61 TGAACAACAGCCAAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCTCTGTTACA 120
Db
QY 2879 TGAAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCTCTGTTACA 2938
QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAATAAGTCTCTCAACAT 180
Db
QY 2939 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAATAAGTCTCTCAACAT 2998
QY 181 TAGGTCCCATTTGGAAGCCAGTCTGTGACAGTGGAGCGTCTGCACTTCTCTGCAGGA 240
Db
QY 2999 TAGGTCCCATTTGGAAGCCAGTCTGTGACAGTGGAGCGTCTGCACTTCTCTGCAGGA 3058
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db
QY 3059 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 3118
QY 301 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGATGATTAAGCCGGCAGGCACCTATTGAA 360
Db
QY 3119 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGATGATTAAGCCGGCAGGCACCTATTGAA 3178
QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db
QY 3179 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 3238
QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACAGGAGCCCCAGAGAGCTGCCTCTCTGAGGAG 480
Db
QY 3239 GCCTTTGGAAGGACTAGAGAAACTCTACAGGAGCCCCAGAGAGCTGCCTCTCTGAGGAG 3298
QY 481 AGCCCAAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db
QY 3299 AGCCCAAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 3358
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAATAAGATGAGACCCCTTGAAAGACT 600
Db
QY 3359 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAATAAGATGAGACCCCTTGAAAGACT 3418

QY 601 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGTGAT 660
Db
QY 3419 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGTGAT 3478
QY 661 CAAGGGATCCTGGCAGCCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
Db
QY 3479 CAAGGGATCCTGGCAGCCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 3538
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGTGAGCCACGTCAA 780
Db
QY 3539 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGTGAGCCACGTCAA 3598
QY 781 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAAACCTCAGCAC 840
Db
QY 3599 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAAACCTCAGCAC 3658
QY 841 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCGCTCGAGGACCGAGTCAG 900
Db
QY 3659 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCGCTCGAGGACCGAGTCAG 3718
QY 901 GCAGCTGCATGAAGCCACACAGGACCTTTGGTCCAGCATCTCAGACATTTCTTTCCACGTC 960
Db
QY 3719 GCAGCTGCATGAAGCCACACAGGACCTTTGGTCCAGCATCTCAGACATTTCTTTCCACGTC 3778
QY 961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA 1020
Db
QY 3779 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA 3838
QY 1021 CGAGACTCAAAACAACTTGTCTGGGACCATCCAAAATGACAGAGCTCTACAGTCTTTTAGC 1080
Db
QY 3839 CGAGACTCAAAACAACTTGTCTGGGACCATCCAAAATGACAGAGCTCTACAGTCTTTTAGC 3898
QY 1081 TGACCTGAATATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA 1140
Db
QY 3899 TGACCTGAATATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA 3958
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTTCAGTGCATGTGATGCTTGGACCAGCA 1200
Db
QY 3959 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTTCAGTGCATGTGATGCTTGGACCAGCA 4018
QY 1201 CAACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCCAC 1260
Db
QY 4019 CAACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCCAC 4078
QY 1261 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
Db
QY 4079 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 4138
QY 1321 TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1380
Db
QY 4139 TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 4198
QY 1381 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAG 1440
Db
QY 4199 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAG 4258
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGGTGGGCCT 1500
Db
QY 4259 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGGTGGGCCT 4318
QY 1501 C 1501
Db 4319 C 4319

RESULT 12
AAD37255
ID AAD37255 standard; DNA; 5149 Bp.
XX
AC AAD37255;
XX
DT 21-AUG-2002 (first entry)

XX DE Adeno-associated virus vector plasmid, AAV-MCK-delta173.
XX KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX OS Homo sapiens.
OS OS Unidentified.
OS OS Chimeric.
XX WO200183695-A2.
PN 08-NOV-2001.
XX 27-APR-2001; 2001WO-US013677.
PF 28-APR-2000; 2000US-0200777P.
XX (XIAO/) XIAO X.
PA Xiao X;
XX WPI; 2002-049342/06.
DR New dystrophin minigene for treating Duchenne or Becker muscular
XX dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX Example 1; Page 57-59; 71pp; English.
PS The present invention relates to an isolated nucleotide sequence encoding
XX a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence
XX Sequence 5149 BP; 1489 A; 1236 C; 1269 G; 1155 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1501; DB 6; Length 5149;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAAGGTGAAATTGAAGCTCACAACAGATGTTTATCACAACCTGGA 60
DB 2908 ACAATGGCAAGACCTCCAAAGGTGAAATTGAAGCTCACAACAGATGTTTATCACAACCTGGA 2967
QY 61 TGAATAACAGCCAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGAGTCCCTGTTACA 120
DB 2968 TGAATAACAGCCAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGAGTCCCTGTTACA 3027
QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 180
DB 3028 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 3087
QY 181 TAGGTCCCATTTGGAAAGCCAGTTCTGTACCACTGGAAGCGTCTGCACCTTCTCTGCAGGA 240
DB 3088 TAGGTCCCATTTGGAAAGCCAGTTCTGTACCACTGGAAGCGTCTGCACCTTCTCTGCAGGA 3147
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAAGCCGGCAGGCACCTATTGGAGG 300
DB 3148 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAAGCCGGCAGGCACCTATTGGAGG 3207
QY 301 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 360
DB

DB 3208 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 3267
QY 361 AACTAAAGAACCTGTAAATCATGAGTACTTGTGAGACTGTACGAATATTTCTGACAGAGCA 420
DB 3268 AACTAAAGAACCTGTAAATCATGAGTACTTGTGAGACTGTACGAATATTTCTGACAGAGCA 3327
QY 421 GCCTTTGGAAAGACTAGAGAAACTCTACAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG 480
DB 3328 GCCTTTGGAAAGACTAGAGAAACTCTACAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG 3387
QY 481 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
DB 3388 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 3447
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 600
DB 3448 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 3507
QY 601 CCAGGAACCTTCAAGAGGCCCACGGATGAGCTGGACCTCAAGCTCGCCCAAGCTGAGGTGAT 660
DB 3508 CCAGGAACCTTCAAGAGGCCCACGGATGAGCTGGACCTCAAGCTCGCCCAAGCTGAGGTGAT 3567
QY 661 CAAGGATCCTGGCAGCCCCTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACCCTCGA 720
DB 3568 CAAGGATCCTGGCAGCCCCTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACCCTCGA 3627
QY 721 GAAAGTCAAGGCACCTTCGAGAGAGAAATTCGCCCTCTGAAAGAGAACGCTGAGCCACGTCAA 780
DB 3628 GAAAGTCAAGGCACCTTCGAGAGAGAAATTCGCCCTCTGAAAGAGAACGCTGAGCCACGTC 3687
QY 781 TGACCTTCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 840
DB 3688 TGACCTTCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 3747
QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAG 900
DB 3748 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAG 3807
QY 901 GCAGCTGCATGAAGCCACAGGGACCTTTGGTTCAGCATCTCAGCATCTTTTCCACGTC 960
DB 3808 GCAGCTGCATGAAGCCACAGGGACCTTTGGTTCAGCATCTCAGCATCTTTTCCACGTC 3867
QY 961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020
DB 3868 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 3927
QY 1021 CGAGACTCAAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTTAGC 1080
DB 3928 CGAGACTCAAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTTAGC 3987
QY 1081 TGACCTGAATAATGTCAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
DB 3988 TGACCTGAATAATGTCAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 4047
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGGCCCTGTGATGATGATGATGATGATGATGATGATGAT 1200
DB 4048 GAAGGCCCTTTGCTTGGATCTCTTGGCCCTGTGATGATGATGATGATGATGATGATGAT 4107
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCTCTGAGCTGTGATGATGATGATGATGATGAT 1260
DB 4108 CAACCTCAAGCAAAATGACAGCCCATGGATATCTCTGAGATTTATTAATTTGTTGACCCAC 4167
QY 1261 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
DB 4168 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 4227
QY 1321 TATGTGTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACCAACAGGAGGATCCGTGT 1380
DB 4228 TATGTGTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACCAACAGGAGGATCCGTGT 4287
QY 1381 CCTGTCTTTTAAACTGGCATCAATTTCCCTGTGTAAAGCACAATTTGGAAGACAAGTACAG 1440
DB 4288 CCTGTCTTTTAAACTGGCATCAATTTCCCTGTGTAAAGCACAATTTGGAAGACAAGTACAG 4347

QY	1261	TATTTATGACCGCTGGAGCAAGAGCACAA	CAATTGGTCAACGTCCCTCTCTCGGTGGA	1320
Db	2953	TATTTATGACCGCTGGAGCAAGAGCACAA	CAATTGGTCAACGTCCCTCTCTCGGTGGA	3012
QY	1321	TATGTGCTGAACCTGGCTGCTGAATGTT	TATGATACGGGACGAACAGGGAGGATCCGTGT	1380
Db	3013	TATGTGCTGAACCTGGCTGCTGAATGTT	TATGATACGGGACGAACAGGGAGGATCCGTGT	3072
QY	1381	CCTGTCTTTTAAACTGGCATCATTTCCCT	GTGTAAAGCACATTTGGAAGACAAGTACAG	1440
Db	3073	CCTGTCTTTTAAACTGGCATCATTTCCCT	GTGTAAAGCACATTTGGAAGACAAGTACAG	3132
QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTTCA	ACAGGATTTTGTGACCGCAGCGTGGGCCT	1500
Db	3133	ATACCTTTTCAAGCAAGTGGCAAGTTTCA	ACAGGATTTTGTGACCGCAGCGTGGGCCT	3192
QY	1501	C	1501	
Db	3193	C	3193	

RESULT 1A

RESOLUTION
ABK81999

ABK81999
ID ABK81999 standard: DNA: 5462 BP.

[illegible]

AC ABK81999:

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DNA encoding

[illegible]

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10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044

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QY	61	TGAAAACAGCCAA	AAAAATCCTGAGAT	CCCTGGAAAGGTT	CCGATGAT	GCAGTCCT	TGTTACA	120		
DB	1876	TGAAAACAGCCAA	AAAAATCCTGAGAT	CCCTGGAAAGGTT	CCGATGAT	GCAGTCCT	TGTTACA	1935		
QY	121	AAGACGTTTGGATA	AACATGAAC	TTCAAGTGGAGT	GAACTTCG	GAAAAAAGTCT	CTCAACAT	180		
DB	1936	AAGACGTTTGGATA	AACATGAAC	TTCAAGTGGAGT	GAACTTCG	GAAAAAAGTCT	CTCAACAT	1995		
QY	181	TAGGTCCCATTTGG	AAGCCAGTTCTG	ACCAGTGGAAAGCGT	CTGCACCT	TTTCTCTGCAGGA	240			
DB	1996	TAGGTCCCATTTGG	AAGCCAGTTCTG	ACCAGTGGAAAGCGT	CTGCACCT	TTTCTCTGCAGGA	2055			
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QY	361	AACTAAAGAACTGT	TAATCATGAGTACT	CTTGAGACTGTACGAAT	TATTTCTGACAGAGCA	420				
DB	2176	AACTAAAGAACTGT	TAATCATGAGTACT	CTTGAGACTGTACGAAT	TATTTCTGACAGAGCA	2235				
QY	421	GCCTTTGGAAGGAC	TAGAGAACTCT	TACCAGGAGCCAGAGAGCT	GCCTCCTCTGAGGAGAG	480				
DB	2236	GCCTTTGGAAGGAC	TAGAGAACTCT	TACCAGGAGCCAGAGAGCT	GCCTCCTCTGAGGAGAG	2295				
QY	481	AGCCACAGAAATGT	CACTCGGCTTCT	ACGAAAGCAGGCT	TGAGGAGGTCAAT	TACTGAGTGGGA	540			
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QY	541	AAAATTGAACCTGC	ACTCCGCTGACT	GGCAGAGAAAAATAG	ATGAGACCCT	TGAAAAGACT	600			
DB	2356	AAAATTGAACCTGC	ACTCCGCTGACT	GGCAGAGAAAAATAG	ATGAGACCCT	TGAAAAGACT	2415			
QY	601	CCAGGAACTTCAAG	AGGGCCACGGAT	GAGCTGGACCTCAAGCT	CGCCAAAGT	TGAGGTGAT	660			
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DB	2536	GAAAGTCAAGGCACT	TCGAGGAGAAAT	TGGCCTCTGAAAGAGAA	ACGTGAGCCACGTCAA	2595				
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QY	841	TCTGGAAGACCTGA	ACCAACAGATGGA	AGCTTCTG	CAGGTGGCCGT	TCGAGGACCGAGT	CAG	900		
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QY	901	GCAGCTGCATGAAG	CCACAGGGACTTT	TGTCAGCATCT	CAGCACTTTCT	TTTCCACGTC	960			
DB	2716	GCAGCTGCATGAAG	CCACAGGGACTTT	TGTCAGCATCT	CAGCACTTTCT	TTTCCACGTC	2775			
QY	961	TGTCCAGGGTCCCT	TGGGAGAGCCAT	CTCGCCAAA	CAAAGTGCCCT	TACTATATCAACCA	1020			
DB	2776	TGTCCAGGGTCCCT	TGGGAGAGCCAT	CTCGCCAAA	CAAAGTGCCCT	TACTATATCAACCA	2835			
QY	1021	CGAGACTCAAA	CAAACTTGCTGGG	ACCATCCAAAAAT	GACAGAGCTCT	ACCAGTCTTTAGC	1080			
DB	2836	CGAGACTCAAA	CAAACTTGCTGGG	ACCATCCAAAAAT	GACAGAGCTCT	ACCAGTCTTTAGC	2895			


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QY 1081 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA 1140
Db 2896 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA 2955
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGACGTCATGTGATGCTTGGACCAGCA 1200
Db 2956 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGACGTCATGTGATGCTTGGACCAGCA 3015
QY 1201 CAACCTCAAGCAAAATGACCAAGCCCATGGATATCTCTGCAGATTATTAAATGTTGACCAC 1260
Db 3016 CAACCTCAAGCAAAATGACCAAGCCCATGGATATCTCTGCAGATTATTAAATGTTGACCAC 3075
QY 1261 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
Db 3076 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 3135
QY 1321 TATGTCCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1380
Db 3136 TATGTCCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 3195
QY 1381 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1440
Db 3196 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 3255
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTGTGACCAAGCGGCTGGGCT 1500
Db 3256 ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTGTGACCAAGCGGCTGGGCT 3315
QY 1501 C 1501
Db 3316 C 3316
RESULT 15
AAD06794
ID AAD06794 standard; DNA; 5952 BP.
XX
AC AAD06794;
XX
DI 06-AUG-2001 (first entry)
XX
DE Human dystrophin gene (Becker form).
XX
KW Human; dystrophin; extein; intein; trans-splicing; gene therapy;
KW Duchenne muscular dystrophy; Becker muscular dystrophy; DMD; BMD; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_recomb 2847..2848
FT /*tag= a
FT /label= S4_junction_site
FT /note= "Dystrophin gene is split at this site and
FT attached to an intein sequence. The resulting fragment is
FT used to produce plasmid pSD4"
FT 2952..2953
FT /*tag= b
FT /label= S3_junction_site
FT /note= "Dystrophin gene is split at this site and
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FT used to produce plasmid pSD3"
FT 3198..3199
FT /*tag= c
FT /label= S2_junction_site
FT /note= "Dystrophin gene is split at this site and
FT attached to an intein sequence. The resulting fragment is
FT used to produce plasmid pSD2"
FT 3300..3301
FT /*tag= d
FT /label= S1_junction_site
FT /note= "Dystrophin gene is split at this site and
FT attached to an intein sequence. The resulting fragment is
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FT XX used to produce plasmid pSD1"
PN WO200129243-A1.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-CA001216.
XX
PR 15-OCT-1999; 99US-0159868P.
XX
PA (UYDA-) UNIV DALHOUSIE.
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Paul XL, Xiao X;
XX WPI; 2001-367297/38.
XX
PT Use of spontaneous or automatic protein splicing to join two or more
PT peptides at junction site involves expressing extein peptides having co-
PT reacting portions of split intein attached to them, so that peptides
PT splice.
XX
PS Example 1; Fig 2; 81pp; English.
XX
CC The invention relates to a method directed to the use of spontaneous or
CC automatic protein trans-splicing to join two or more peptides at junction
CC site. This method involves expressing extein peptides having co-reacting
CC portions of split intein attached to them, so that peptides will splice
CC automatically under suitable conditions. The invention also provides
CC methods for circumventing virion packaging size limitations in
CC recombinant virus particle, by splitting a coding region for a protein to
CC be delivered into two or more extein genes, which are packaged in
CC separate virus particles and are co-delivered in a target cell for the
CC expression and for subsequent trans-splicing to form the complete
CC protein. In particular, the method is used for trans-splicing human
CC dystrophin and in gene therapies of recombinant adeno-associated virus
CC (AAV) particles that encode trans-spliced dystrophin, for treating
CC diseases such as Duchenne muscular dystrophy (DMD) or Becker muscular
CC dystrophy (BMD). The present sequence is human dystrophin gene (Becker
CC form)
XX
SQ Sequence 5952 BP; 1860 A; 1344 C; 1410 G; 1338 T; 0 U; 0 Other;
Query Match 100.0%; Score 1501; DB 5; Length 5952;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAAGGTGAATTAAGCTCACACAGATGTTTATCACAACTGGA 60
Db 3102 ACAATGGCAAGACCTCCAAAGGTGAATTAAGCTCACACAGATGTTTATCACAACTGGA 3161
QY 61 TGAACAACAGCCAAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCCCTGTACA 120
Db 3162 TGAACAACAGCCAAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCCCTGTACA 3221
QY 121 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTCGAAAAAGTCTCTCAACAT 180
Db 3222 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTCGAAAAAGTCTCTCAACAT 3281
QY 181 TAGGTCCCATTTGGAAGCCAGTTCTGACCAAGTGGAGGCTCTGCACCTTTCTCTGCAGGA 240
Db 3282 TAGGTCCCATTTGGAAGCCAGTTCTGACCAAGTGGAGGCTCTGCACCTTTCTCTGCAGGA 3341
QY 241 ACTTCTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCCGGAGGACCTATTGGAGG 300
Db 3342 ACTTCTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCCGGAGGACCTATTGGAGG 3401
QY 301 CGACTTTTCCAGCAGTTTCAAGAGCAGAACCGATGTACATAGGGCTTCAAGAGGGAATTGAA 360
Db 3402 CGACTTTTCCAGCAGTTTCAAGAGCAGAACCGATGTACATAGGGCTTCAAGAGGGAATTGAA 3461
QY 361 AACTAAAGAACCTGTATCATGAGTACTCTTGGAGACTCTGACCAATATTTCTGACAGAGCA 420
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Db	3522	GCCTTTTGAAGGACTAGAGAAACTCTACAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG	3581
QY	481	AGCCAGAAATGTCACTCGGCTTCTACGAAGACAGGCTGAGGAGGTCAATACTAGTGGGA	540
Db	3582	AGCCAGAAATGTCACTCGGCTTCTACGAAGACAGGCTGAGGAGGTCAATACTAGTGGGA	3641
QY	541	AAAATTGAACCTCGACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAAAGACT	600
Db	3642	AAAATTGAACCTCGACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAAAGACT	3701
QY	601	CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGAT	660
Db	3702	CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGAT	3761
QY	661	CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGAGCTCTCTCCAAGATCACCTCGA	720
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QY	721	GAAAGTCAAGGCACCTTCGAGGAGAGAAATTCGCCCTCTGAAAGAGAAACGTGAGCCACGTCAA	780
Db	3822	GAAAGTCAAGGCACCTTCGAGGAGAGAAATTCGCCCTCTGAAAGAGAAACGTGAGCCACGTCAA	3881
QY	781	TGACCTTGCTCGCCAGCTTACCCTTTTGGGCATTCAGCTCTCACCGTATACCTCAGCAC	840
Db	3882	TGACCTTGCTCGCCAGCTTACCCTTTTGGGCATTCAGCTCTCACCGTATACCTCAGCAC	3941
QY	841	TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCCGTTCGAGGACCGAGTCAG	900
Db	3942	TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCCGTTCGAGGACCGAGTCAG	4001
QY	901	GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC	960
Db	4002	GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC	4061
QY	961	TGTCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA	1020
Db	4062	TGTCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA	4121
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QY	1081	TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA	1140
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QY	1141	GAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGACCAGCA	1200
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QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTACACAGCCAGGCTGGGCCT	1500
Db	4542	ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTACACAGCCAGGCTGGGCCT	4601

QY 1501 C 1501
Db 4602 C 4602

Search completed: September 19, 2004, 04:48:54
Job time : 413.027 secs

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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 03:01:40 ; Search time 77.4052 Seconds
(without alignments)
10761.315 Million cell updates/sec

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	63.6	4.2	238	4	US-09-687-875A-13
9	53.4	3.6	7218	1	US-08-232-463-14
10	44.2	2.9	2574	4	US-09-668-313A-10
11	42.8	2.9	1690	4	US-09-620-312D-69
12	42.8	2.9	7812	3	US-09-368-590-1
13	38.6	2.6	1995	1	US-08-425-069-3
14	38.6	2.6	1995	2	US-08-317-844B-3
15	38.4	2.6	7672	4	US-09-220-132-24
16	38.2	2.5	428	4	US-09-668-313A-3
17	38.2	2.5	4439	4	US-09-668-313A-17
18	35	2.3	2169	4	US-09-434-408-3
19	34.6	2.3	474	4	US-09-621-976-18033
C 20	34.6	2.3	2277	1	US-08-676-967-5
C 21	34.6	2.3	2277	1	US-08-676-974-5
C 22	34.6	2.3	2277	2	US-09-098-487-5
23	34.6	2.3	246240	2	US-08-724-394A-20
24	34.6	2.3	246240	2	US-08-724-394A-21
25	34.6	2.3	246240	2	US-08-724-394A-22
26	34.4	2.3	1047	4	US-09-671-950-1
27	34.4	2.3	1047	4	US-09-671-950-3

28	34.4	2.3	1047	4	US-09-671-950-5	Sequence 5, Appli
29	34.4	2.3	1047	4	US-09-671-950-7	Sequence 7, Appli
30	34.4	2.3	1047	4	US-09-671-950-9	Sequence 9, Appli
31	34.4	2.3	1047	4	US-09-671-950-11	Sequence 11, Appli
32	34.4	2.3	1047	4	US-09-671-950-13	Sequence 13, Appli
33	34.4	2.3	750	4	US-08-961-527-370	Sequence 370, App
34	34.2	2.3	1620	4	US-08-858-207A-56	Sequence 56, Appli
35	34.2	2.3	2800	2	US-08-874-138-1	Sequence 1, Appli
36	34.2	2.3	2800	2	US-08-874-138-5	Sequence 5, Appli
37	34.2	2.3	2800	3	US-08-879-941-1	Sequence 1, Appli
38	34.2	2.3	2800	3	US-08-879-941-3	Sequence 3, Appli
39	34.2	2.3	2800	4	US-09-747-116-1	Sequence 1, Appli
40	34.2	2.3	2800	4	US-09-747-116-3	Sequence 3, Appli
41	34.2	2.3	32768	4	US-08-961-527-71	Sequence 71, Appli
42	34	2.3	648	4	US-09-252-991A-10033	Sequence 10033, A
C 43	34	2.3	762	4	US-09-252-991A-9821	Sequence 9821, Ap
44	34	2.3	1644	4	US-09-252-991A-10161	Sequence 10161, A
C 45	34	2.3	2235	3	US-09-153-804-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-687-875A-1
; Sequence 1, Application US/09687875A
; Patent No. 6544786
; GENERAL INFORMATION:
; APPLICANT: Xiao, Xiao
; APPLICANT: Liu, Paul
; TITLE OF INVENTION: METHOD AND VECTOR FOR PRODUCING AND TRANSFERRING TRANS-SPLICED P
; FILE REFERENCE: 00792
; CURRENT APPLICATION NUMBER: US/09/687,875A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/158,868
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2897)..(2898)
; OTHER INFORMATION: S4 junction site
; NAME/KEY: misc feature
; LOCATION: (3198)..(3199)
; OTHER INFORMATION: S2 junction site
US-09-687-875A-1

Query Match 100.0%; Score 1501; DB 4; Length 5952;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACTGGA	60
Db	3102	ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACTGGA	3161
Qy	61	TGAAACAGCCAAAAATCCTGAGATCCCTGGAGGTTCCGATGATGCAGTCCTGTTACA	120
Db	3162	TGAAACAGCCAAAAATCCTGAGATCCCTGGAGGTTCCGATGATGCAGTCCTGTTACA	3221
Qy	121	AAGACGTTGGATAACATGAATTCAAGTGGAGTGAACCTCGGAAAAAGTCTCTCAACAT	180
Db	3222	AAGACGTTGGATAACATGAATTCAAGTGGAGTGAACCTCGGAAAAAGTCTCTCAACAT	3281
Qy	181	TAGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA	240
Db	3282	TAGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA	3341
Qy	241	ACTTCTGGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG	300

Db 3342 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 3401

QY 301 CGACTTTCCAGCAGTTTCAAGACGAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 360

Db 3402 CGACTTTCCAGCAGTTTCAAGACGAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 3461

QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420

Db 3462 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 3521

QY 421 GCCTTTGGAAGGACTAGAGAACTCTACAGAGAGCCCGAGAGCTGCCTCCTGAGGAGAG 480

Db 3522 GCCTTTGGAAGGACTAGAGAACTCTACAGAGAGCCCGAGAGCTGCCTCCTGAGGAGAG 3581

QY 481 AGCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATACTAGTGGGA 540

Db 3582 AGCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATACTAGTGGGA 3641

QY 541 AAAATTGAACCTGCACTCCGCTGACTGSCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 600

Db 3642 AAAATTGAACCTGCACTCCGCTGACTGSCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 3701

QY 601 CCAGGAACCTTCAAGAGGCCACGGATGAGTGGACCTCAAGCTCGGCCAAGCTGAGGTGAT 660

Db 3702 CCAGGAACCTTCAAGAGGCCACGGATGAGTGGACCTCAAGCTCGGCCAAGCTGAGGTGAT 3761

QY 661 CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720

Db 3762 CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 3821

QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGCTGAGCCACGTCAA 780

Db 3822 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGCTGAGCCACGTCAA 3881

QY 781 TGACCTTGCTGCCAGCTTACCATTGCGCATTCAGCTCTCACCGTATAACCTCAGCAC 840

Db 3882 TGACCTTGCTGCCAGCTTACCATTGCGCATTCAGCTCTCACCGTATAACCTCAGCAC 3941

QY 841 TCTGGAAGACCTGAAACACAGATGGAAGCTTCTGCAGGTGGCCGCTCGAGGACCGAGTCAG 900

Db 3942 TCTGGAAGACCTGAAACACAGATGGAAGCTTCTGCAGGTGGCCGCTCGAGGACCGAGTCAG 4001

QY 901 GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTCTTCTTCACCGTC 960

Db 4002 GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTCTTCTTCACCGTC 4061

QY 961 TGTCCAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020

Db 4062 TGTCCAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 4121

QY 1021 CGAGACTCAAAACAACTTGTGTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080

Db 4122 CGAGACTCAAAACAACTTGTGTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 4181

QY 1081 TGACCTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAAGACTGCA 1140

Db 4182 TGACCTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAAGACTGCA 4241

QY 1141 GAAGSCCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGAGCCTGTGATGCCITGGACCCAGCA 1200

Db 4242 GAAGSCCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGATGCCITGGACCCAGCA 4301

QY 1201 CAACCTCAAGCAAAATGACCAAGCCCATGGATATCCCTGCAGATTATTAATTGTTGACCCAC 1260

Db 4302 CAACCTCAAGCAAAATGACCAAGCCCATGGATATCCCTGCAGATTATTAATTGTTGACCCAC 4361

QY 1261 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGGA 1320

Db 4362 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGGA 4421

QY 1321 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380

Db 4422 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 4481

QY 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1440

Db 4482 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 4541

QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACAGCGCAGGCTGGCCT 1500

Db 4542 ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACAGCGCAGGCTGGCCT 4601

QY 1501 C 1501

Db 4602 C 4602

RESULT 2

US-09-484-970B-60
; Sequence 60, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 60
; LENGTH: 13977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 229357.11CB1
; NAME/KEY: unsure
; LOCATION: 11721-11761, 12294, 13969
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-60

Query Match 99.8%; Score 1497.4; DB 4; Length 13977;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAATGSCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACACCTGGA 60

Db 8416 ACAATGSCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACACCTGGA 8475

QY 61 TGAACACAGCCAAATAATCTCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 120

Db 8476 TGAACACAGCCAAATAATCTCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 8535

QY 121 AAGACGTTTGGATAACATGAATACTCAAGTGGAGTGAATTCGGAAAAAGTCTCTCAACAT 180

Db 8536 AAGACGTTTGGATAACATGAATACTCAAGTGGAGTGAATTCGGAAAAAGTCTCTCAACAT 8595

QY 181 TAGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 240

Db 8596 TAGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 8655

QY 241 ACTTCTGGTGTGGCTACAGTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300

Db 8656 ACTTCTGGTGTGGCTACAGTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 8715

QY 301 CGACTTTCCAGCAGTTTCAAGAGCAGAACCGATGTACATAGGGCCTTCAAGAGGGAATTGAA 360

Db 8716 CGACTTTCCAGCAGTTTCAAGAGCAGAACCGATGTACATAGGGCCTTCAAGAGGGAATTGAA 8775

QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420

Db 8776 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 8835

QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCAGAGAGCTGCCTCTGAGGAGAG 480

Db 8836 GCCTTTGGAAGGACTAGAGAACTCTACGAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 8895
Qy 481 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGAGGTCAATACTAGTGGGA 540
Db 8896 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGAGGTCAATACTAGTGGGA 8955
Qy 541 AAAATTGAACCTGCACCTCCGCTGACTCGGCTGAGAGAGAGAAATAGATGAGACCTTTGAAAGACT 600
Db 8956 AAAATTGAACCTGCACCTCCGCTGACTCGGCTGAGAGAGAGAAATAGATGAGACCTTTGAAAGACT 9015
Qy 601 CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGTCGCGCCAAAGCTGAGTGAT 660
Db 9016 CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGTCGCGCCAAAGCTGAGTGAT 9075
Qy 661 CAAGGATCCTGGCAGCCCGTGGGCGATCTCCTCAATTGACTCTCTCCAAGATCACCTCGA 720
Db 9076 CAAGGATCCTGGCAGCCCGTGGGCGATCTCCTCAATTGACTCTCTCCAAGATCACCTCGA 9135
Qy 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCTCTGAAAGAGAACTGAGCCACGTCAA 780
Db 9136 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCTCTGAAAGAGAACTGAGCCACGTCAA 9195
Qy 781 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCAC 840
Db 9196 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCAC 9255
Qy 841 TCTGGAAGACTGAACACACAGATGGAAGCTTCTGCAGGTGGCGTCGAGGACCGAGTCAG 900
Db 9256 TCTGGAAGACTGAACACACAGATGGAAGCTTCTGCAGGTGGCGTCGAGGACCGAGTCAG 9315
Qy 901 GCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 960
Db 9316 GCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 9375
Qy 961 TGTCCAGGTCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGGCCCTACTATATCAACCA 1020
Db 9376 TGTCCAGGTCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGGCCCTACTATATCAACCA 9435
Qy 1021 CGAGACTCAAAACAACTTGTGGGACCATCCCAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db 9436 CGAGACTCAAAACAACTTGTGGGACCATCCCAAATGACAGAGCTCTACCAGTCTTTAGC 9495
Qy 1081 TGACCTGAATAATGTCAAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 9496 TGACCTGAATAATGTCAAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 9555
Qy 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGCAGTGCATGTGATGCCTTTGGACCA 1200
Db 9556 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGCAGTGCATGTGATGCCTTTGGACCA 9615
Qy 1201 CAACCTCAAGCAAAATGACCAAGCCATGGATATCCTGCAGATTATTAATTGTTGACCA 1260
Db 9616 CAACCTCAAGCAAAATGACCAAGCCATGGATATCCTGCAGATTATTAATTGTTGACCA 9675
Qy 1261 TATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGA 1320
Db 9676 TATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGA 9735
Qy 1321 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGACAGGGAGGATCCGTGT 1380
Db 9736 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGACAGGGAGGATCCGTGT 9795
Qy 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1440
Db 9796 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 9855
Qy 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGCC 1499
Db 9856 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGCC 9914

RESULT 3

US-08-836-022A-10/c
; Sequence 10, Application US/08836022A
; Patent No. 6001557
; GENERAL INFORMATION:
; APPLICANT: Trustees of the University of Pennsylvania
; APPLICANT: Wilson, James M.
; APPLICANT: Fisher, Krishna J.
; APPLICANT: Chen, Shu-Jen
; APPLICANT: Weitzman, Matthew
; TITLE OF INVENTION: Improved Adenovirus Virus and
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,022A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,381
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GNVN.008PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-836-022A-10

Query Match 86.5%; Score 1298.4; DB 3; Length 19307;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 1 ACAATGGCAAGACCTCCAAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGA 60
Db 6278 ACCATGGCAAGATCTCCAAGGAGAAATTGAAACTCACACAGATATCTATCACAATCTTGA 6219
Qy 61 TGAAACACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCACTCCTGTTACA 120
Db 6218 TGAAATGGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGGAAGCAACCCCTGTTACA 6159
Qy 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 180
Db 6158 AAGACGTTTGGATAACATGAATTTCAAGTGGAGTGAACCTTCAGAAAAAGTCTCTCAACAT 6099
Qy 181 TAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 6098 TAGGTCCCATTTGGAAGCAAGTTCTGACCAGTGAAGCGTTTGCATCTTTCTCTTCAGGA 6039
Qy 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db 6038 ACTTCTTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGTCAAGGCCCATCGGTGG 5979
Qy 301 CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTATACATAGGCGCTTCAAGAGGGAATTGAA 360
Db 5978 TGATTTCCAGCAGTTTCAAGAGCAGAAATGATATACATAGGCGCTTCAAGAGGGAATTGAA 5919

QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGGCA 420
Db 5918 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTGAGAATATTTCTGACAGGCA 5859

QY 421 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGTGCCTCCTGAGGAGAG 480
Db 5858 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGTGCCTCCTGGAAGAAAG 5799

QY 481 AGCCAGAAATGTCACCTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db 5798 AGCTCAGAAATGTCACCTCGGCTCCTACGAAGCAGGCTGAAGAGGTCAACGCTGAATGGGA 5739

QY 541 AAAATTGAACCTGCACCTCCGCTGACTGCGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 600
Db 5738 CAAATTGAACCTGCGCTCAGCTGATTTGGCAGAGAAAAATAGATGAAGCTCTTGAAAGACT 5679

QY 601 CCAGGAACCTTAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGAT 660
Db 5678 CCAGGAACCTTAAGAGGCCACGGATGAGCTGGACCTCAAGTTGCGCCCAAGCTGAGGTGAT 5619

QY 661 CAAGGATCTGCGCAGCCCGTGGCGATCTCCTCATTTGAGTCTCTCCAAGATCACTCGA 720
Db 5618 CAAGGATCTGCGCAGCCCGTGGCGATCTCCTCATTTGAGTCTCTCCAAGATCACTCGA 5559

QY 721 GAAAGTCAAGGCACTTCGAGGAGAAATGCGCCTCTGAAAGAGAACTGAGCCACGTCAA 780
Db 5558 AAAAGTCAAGGCACTTCGAGGAGAAATGCGCCTCTTAAAGAGAAATGTCATCGTGTCAA 5499

QY 781 TGACCTTGCTCGCCAGCTTACCATTGTTGGCATTCTCAGCTCTCACCGTATAACCTCAGCAC 840
Db 5498 TGACCTTGACATCAGCTGACCACTGCGCATTCAGCTCTCACCTTATAACCTCAGCAC 5439

QY 841 TCTGGAAGACCTGAAACACCAAGATGGAAGCTTCTGAGGTGGCGCTCGAGGACCGAGTCA 900
Db 5438 TTTGGAAGATCTGAATACCAGATGGAGGCTTCTACAGGTGGCTGTGGAGGACCGGTGTCAG 5379

QY 901 GCAGCTGCATGAAGCCCAACAGGAGCTTGGTCCAGCATCTCAGCACCTTCTTCCACGTC 960
Db 5378 ACAGCTGCATGAAGCCCAACAGGAGCTTGGTCCAGCATCTCAGCACCTTCTTCCACCTTC 5319

QY 961 TGTCAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCA 1020
Db 5318 AGTTGAGGTCCCTGGGAGAGAGCCATCTCACCACAAAGTCCCTACTATATCAACCA 5259

QY 1021 CGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGC 1080
Db 5258 CGAGACCAAAACCACTTGTTGGGACCAACCCCAAAATGACAGAGCTCTACCACTCTTTAGC 5199

QY 1081 TGACCTGAATAATGTGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAGAGACTGCA 1140
Db 5198 TGACCTGAATAATGTGATTTCTCGCGTATAGGACTGCCATGAAACTCCGAGAGCTCCA 5139

QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCTTGACCCAGCA 1200
Db 5138 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCTTGACCCAGCA 5079

QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGAGATTTAATGTTGTTGACCCAC 1260
Db 5078 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGAGATTTAATGTTGTTGACTAC 5019

QY 1261 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
Db 5018 AATTATGATCGTCTGGAGCAAGAGCAACAATCTGGTCAATGTCCCTCTCTGTGTGA 4959

QY 1321 TATGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1380
Db 4958 TATGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 4899

QY 1381 CCTGTCTTTAAAACTGGCATCATTTCCCTGTGTGAAGCACATTTGGAAGACAAGTACAG 1440
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QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACAGCGCAGGCTGGGCT 1500
Db 4838 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACAGCGTAGGCTGGGTCT 4779

RESULT 4
US-09-427-048A-10/c
; Sequence 10, Application US/09427048A
; Patent No. 6203975
; GENERAL INFORMATION:
; APPLICANT: Trustees of the University of Pennsylvania
; Wilson, James M.
; Fisher, Krishna J.
; Chen, Shu-Jen
; Weitzman, Matthew
; TITLE OF INVENTION: Improved Adenovirus Virus and
; Methods of Use Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/427,048A
; FILING DATE: 21-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,022
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GNVN.008PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-427-048A-10

Query Match 86.5%; Score 1298.4; DB 3; Length 19307;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 1 ACATGGCAAGACCTCCCAAGGTGAAATTTGAAGCTCACACAGATGTTTATCACAACTTGA 60
Db 6278 ACATGGCAAGATCTCCCAAGGAGAAATTTGAAACTCACACAGATATCTATCACAACTTGA 6219

QY 61 TGAATAACAGCCAAATAATCTGAGATCCCTGGAAGTTCGATGATGATGATGATGATGATGAT 120
Db 6218 TGAATAAGCCAAATAATCTGAGATCCCTGGAAGTTCGATGATGATGATGATGATGATGAT 6159

QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 180
Db 6158 AAGACGTTTGGATAACATGAATTTCAAGTGGAGTGAACCTTCAGAAAAAGTCTCTCAACAT 6099

QY 181 TAGGTCCCATTTGGAAGCCAGTTCTTGACCAAGTGAAGCGTCTGCACTTTCTCTGCAGGA 240
Db 6098 TAGGTCCCATTTGGAAGCAAGTTCTTGACCAAGTGAAGCGTCTTCTCTCTTCAGGA 6039

QY	302	GACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCTTCAAGAGGAAATTGAAA	361
Db	3506	GATGTTCCAGCCTTACAGCTCCAGTATGACCATTTGTAAGGCGCTGAGACGGGAGTTAAAG	3565
QY	362	ACTAAGAAACCTGTAATCATGAGTACTTTTGAGACTGTACGAATATTTCTGACAGAGCAG	421
Db	3566	GAGAAAGAAATATTTCTGCTGAAATGCTGTCGACCAGGCCCGAGTTTCTTGGCTGATCAG	3625
QY	422	CTTTT-----GGAAGGACTAGAGAAACTCTACCAGGAGCCAGAGAGCTGCCTCCT	472
Db	3626	CCAAATTGAGGCCCTGAAGAGCCCAAGAAGAAACCTACAATCAAAAACAGAAATTAATCCT	3685
QY	473	GAGGAGAGAGCCCGAGAAATGTCACTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACT	532
Db	3686	GAGGAGAGAGCCCAAAAGATTGCCAAAGCCATGCGCAAAACAGTCTTCTGAGTCAAGAA	3745
QY	533	GAGTGGGAAAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTT	592
Db	3746	AAATGGGAAAGTCTAAATGCTGTAACTAGCAATTGGCAAAAAGCAAGTGGACAAGGCATTG	3805
QY	593	GAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCT	652
Db	3806	GAGAAACTCAGAGACCTGCAGGGAGCTATGGATGACCTGGACGCTGACATGAAGAGGCA	3865
QY	653	GAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCTCATTTGACTCTCTCCAAGAT	712
Db	3866	GAGTCCGTGCGGAATGGCTGGAAAGCCCGTGGAGACTTACTCATTTGACTCGCTGCAGGAT	3925
QY	713	CACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGC	772
Db	3926	CACATTGAAAAAATCATGGCATTTAGAGAAGAAATTGCACCAATCAACTTTAAAGTTAAA	3985
QY	773	CACGTCAATGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAAC	832
Db	3986	ACGGTGAATGATTTATCCAGTCAGCTGTCTCCACTTGACCTGCATCCCTCTCTAAAAGATG	4045
QY	833	CTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCGTCGAGGAC	892
Db	4046	TCTCGCCAGCTAGATGACCTTAATATCGATGGAACCTTTACAGGTTTCTGTGGATGAT	4105
QY	893	CGAGTCAGGCAGCTGCATGAAGCCCAACAGGCACTTTGGTCCAGCATCTCAGCACTTTCTT	952
Db	4106	CGCCTTAAACAGCTTCAGGAAGCCCAACAGAGATTTTGGACCATCTCTCTCAGCATTTTCTC	4165
QY	953	TCCACGTTCTGCCAGGTCCCTGGGAGAGAGCCCATCTGCCAAACAAAGTCCCTACTAT	1012
Db	4166	TCTACGTCAGTCCAGCTGCCGTGGCAAGATCCATTTACATAATAAAGTGCCTATTAC	4225
QY	1013	ATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAG	1072
Db	4226	ATCAACCATCAAAACACAGACCACCTGTTGGGACCATCCTAAATGACCGAACTCTTTCAA	4285
QY	1073	TCTTTAGCTGACCTGNAATAATGTTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGA	1132
Db	4286	TCCCTTGCTGACCTGAATAATGTACGTTTTTCTGCCTACCGTACAGCAATCAAAATCCGA	4345
QY	1133	AGACTGCAGAAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTTCAGCTGATGTGATGCCTTG	1192
Db	4346	AGACTACAAAAAGCACTATGTTTGGATCTCTTAGAGTTGAGTACAACAAAATGAAATTTTC	4405
QY	1193	GACCAGCACAACTCAAGCAAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGT	1252
Db	4406	AAACAGCACAAAGTTGAACCAAAATGACCAGCTCCTCAGTGTTCAGATGTCTCAACTGT	4465
QY	1253	TTGACCACCTATTTATGACCGCCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTC	1312
Db	4466	CTGACAAACAACCTTATGATGGACTTGAGCAAAATGCATAAGGACCTGGTCAACGTTCCACTC	4525
QY	1313	TGCGTGGATATGTGTCTGAACCTGGCTGTCTGAATGTTTTATGATACGGGACGAACAGGAGG	1372
Db	4526	TGTGTTGATATGTCTCAATTGGTTGCTCAATGTCTATGACACGGGTGCAACTGGAAAA	4585
QY	1373	ATCCGTGCTCTGCTTTTAAAAACTGGCATCATTTCCCTGTGTAAGACACATTTGGAAGAC	1432

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Db      4586  ATTAGAGTGCAGAGCTCTGAAGATTGGATTAAATGTCTCTCTCCAAAGGTCTCTTTGGAAGAA 4645
QY      1433  AAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGG 1492
Db      4646  AAATACAGATATCTCTTTAAGGAAGTTGCGGGGCCGACAGAAATGTGTGACCAAGGCAG 4705
QY      1493  CTGGGCGCT 1500
Db      4706  CTGGGCGCT 4713

RESULT 6
US-09-091-501B-9
; Sequence 9, Application US/09091501B
; Patent No. 6518413
; GENERAL INFORMATION:
; APPLICANT: Tinsley, Jonathon M
; APPLICANT: Davies, Kay E
; TITLE OF INVENTION: Utrophin gene expression
; FILE REFERENCE: 620-42
; CURRENT APPLICATION NUMBER: US/09/091,501B
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: PCT/GB96/03156
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: GB 9525962.8
; PRIOR FILING DATE: 1995-12-19
; PRIOR APPLICATION NUMBER: GB 9615797.9
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: GB 9622174.2
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 10320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(10312)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full length
; OTHER INFORMATION: utrophin construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (724)..(758)
; OTHER INFORMATION: Precise residue is left open
US-09-091-501B-9

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Query Match 40.3%; Score 604.8; DB 4; Length 10320;
Best Local Similarity 63.1%; Pred. No. 1.5e-187;
Matches 952; Conservative 0; Mismatches 547; Indels 9; Gaps 1;

QY 302 GACTTTCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAAA 361
Db |||||
7781 GATGTTCCAGCCTTACAGCTCCAGTATGACCAATTGTAAAGCCCTGAGACGGGAGTTAAAG 7840
QY 362 ACTAAAGAACCTGTAAATCATGATGACTCTCTTGAGACTGTACGAATATTTCTGACAGAGCAG 421
Db |||||
7841 GAGAAAGAAATATTCTGTCTCTGAATGCTGTGCGAACCGCCGAGTTTTCTTGGCTGATCAG 7900
QY 422 CCTTT-----GGAAGGACTAGAGAAAACCTTACCAGGAGCCCGAGAGAGCTGCCCTCCT 472
Db |||||
7901 CCAATTGAGGCGCCCTGAAGAGGCCAAGAGAAACCTACAATCAAAAACAGAAATTAACCTCT 7960
QY 473 GAGGAGAGAGCCCGAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACT 532
Db |||||
7961 GAGGAGAGAGCCCGAAAGATTGCCAAAGCCCATGCGCAAAACAGTCTTCTGAAGTCAAGAA 8020
QY 533 GAGTGGGAAAAAATTGAACCTGCACCTCGCTGACTGCGCAGAGAAAAAATAGATGAGACCCCT 592
Db |||||
8021 AAATGGGAAAGTCTAAATGCTGTAACTAGCAATTGGCAAAAGCAAGTGGACAAGGCATTG 8080
QY 593 GAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCT 652
Db |||||
8081 GAGAAACTCAGAGACCTGCAGGGAGCTATGATGACCTGGACGCTGACATGAAGGAGGCA 8140
QY 653 GAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAGAT 712
Db |||||
8141 GAGTCCGTGGGAATGGCTGGAAGCCCTGGGAGACTTACTCATTTGACTCGCTGCAGGAT 8200
QY 713 CACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACGTGAGC 772
Db |||||
8201 CACATTGAAAAAATCATGGCATTTAGAGAGAAATTGCAACCAATCAACTTTAAAGTTAAA 8260
QY 773 CAGTCAATGACCTTGCTGCCAGCTTACCACCTTTGGGCATTTGAGCTCTCACCGTATAAC 832
Db |||||
8261 ACGGTGAATGATTTATCCAGTCAGCTGTCTCCACTTGACCTGCATCCCTCTCTAAAGATG 8320
QY 833 CTCAGCACTCTGGAAGACCTGAACACCAAGATGGAAGCTTCTGAGGTGGCCGTGAGGAC 892
Db |||||
8321 TCTGCCAGCTAGATGACCTTAATATGCGATGGAAACTTTTACAGGTTTCTGTGGATGAT 8380
QY 893 CGAGTCAGGCAGTGCATGAAGCCCAAGGCCCTTTGGTCCAGATCTCAGCACTTTCTT 952
Db |||||
8381 CGCCTTAAACAGCTTCAGGAAGCCCAAGAGATTTTGGACCATCTCTCTCAGCATTTTCTC 8440
QY 953 TCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCAAACAAAGTGCCCTACTAT 1012
Db |||||
8441 TCTACGTGCTCAGCTGCCGTGGCGTGGCAAGATCCATTTACATAATAAAGTGCCCTATTAC 8500
QY 1013 ATCAACCACGAGACTCAAAACAACCTTGCTGGAGACCATCCCAAAATGACAGAGCTCTACCAG 1072
Db |||||
8501 ATCAACCATCAAAACACAGACCACTGTTGGGACCATCTTAAATGACCGAACTCTTTCAA 8560
QY 1073 TCTTTAGCTGACCTGAATAATGTGATCTCAGCTTATAGGACTGCGCATGAAACTCCGA 1132
Db |||||
8561 TCCCTTGCTGACCTGAATAATGTACGTTTTTCTGCTACCGTACAGCAATCAAAATCCGA 8620
QY 1133 AGACTGCAGAAGGCCCTTTGCTTGGATCTCTGAGCCTGTGACGTGATGATGCCCTTG 1192
Db |||||
8621 AGACTACAAAAGCACTATGTTTGGATCTCTTAGAGTTGAGTACAAACAATGAAATTTT 8680
QY 1193 GACCAGCACAACTCAGCAAAATGACCCAGCCCATGGATATCCTGACGATTTAATTGT 1252
Db |||||
8681 AAACAGCACAAAGTTGAACCAAAATGACCAGCTCTCAGTGTCTCCAGATGTCATCAACTGT 8740
QY 1253 TTGACCACTATTTATACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTC 1312
Db |||||
8741 CTGACAACAACCTTATGATGGACTTGAGCAAAATGCATAAGGACCTGGTCAACGTTCCACTC 8800
QY 1313 TCGCTGGATATGTGCTGAACCTGGCTGTGAATGTTTATGATACGGGACCAACAGGGAGG 1372
Db |||||
8801 TGTGTTGATATGTGCTCAATTTGGTTGCTCAATGTCTATGACACGGGTGAACTGGAAAA 8860
QY 1373 ATCCGTGTCCTGCTTTTAAAACTGGCATCAATTTCCCTGTGTAAAGCACATTTTGAAGAC 1432

Db 8861 ATTAGAGTGCAGAGTCTGAAGATTGGATTAATGTCTCTCTCCAAGGTCTCTTGGAAAGAA 8920
QY 1433 AAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGG 1492
Db |||||
8921 AAATACAGATATCTCTTTAAGGAAGTTGCGGGCCGACAGAAAATGTGTGACCAGAGGCAG 8980
QY 1493 CTGGGCCT 1500
Db |||||
8981 CTGGGCCT 8988

RESULT 7

US-09-976-594-93
; Sequence 93, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 93
; LENGTH: 3915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 290344.1
US-09-976-594-93

Query Match 35.0%; Score 524.8; DB 4; Length 3915;
Best Local Similarity 62.0%; Pred. No. 1.6e-161;
Matches 847; Conservative 0; Mismatches 517; Indels 2; Gaps 1;

QY 136 CATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACATTAGTCCCATTTGGA 195
Db |||||
544 CATGAATCTGTGTGGAAATGAATAAAAAAAGTCTCAACCTCCGCGCTCGCCTAGA 603
QY 196 AGCCAGTTCTGACCAGTGAAGCGTCTGACCTTTCTGACGGAACCTTCTGCTGGTGTGGCT 255
Db |||||
604 GGCCTTCTCAGACCCACAGTGGAAAGCTTCAGCTCCCTCTTCAAGAGATTATTGACTGGCT 663
QY 256 ACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTCCAGCAGT 315
Db |||||
664 CAGCCAAAAGGATGAGAGTTGTCAAGCTCAGCTGCCCTACAGGGGGATGTGGCCCTGGT 723
QY 316 TCAGAAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAAAACATAAGAACCTGT 375
Db |||||
724 GCAACAGGAGAAAGGAGACACATCGGCGCTTTATGGAAGAAAGTCAAGTCTCGGGGCCCTA 783
QY 376 AATCATGAGTACTCTTCAGACTGTACGAATATTTCTGACAGAGCGCTTTGGAAGGACT 435
Db |||||
784 CATCTATTCTGTGCTGGAGTCAGCTCAGGCGCTTCTGTCCAGCACCCATTGAGGAGTT 843
QY 436 AGAGAAAACCTTACCAGGAGCCCGAGAGAGTGCCTCCTGAGGAGAGAGCCCAAGATGTCAC 495
Db |||||
844 AGAGGAGCGCTCATTTCTGAGAGCAAAAGATACCTCCCGAAAAACAGCGGATCCAGAAATCTCAG 903
QY 496 TCGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAAAATTTGAACCTGCA 555
Db |||||
904 CCGCTTGTATGGAAGCAGGCGACGGTGGCCAGTGAAGTGTGGGAGAAAGTTGACAGCCCG 963
QY 556 CTCGCTGACTGGCAGAGAAAAATAGATGAGACCTTGAAGACTCCAGGAACTTCAAGA 615
Db |||||
964 CTGTGTGACCAAGCACCCGTCACATTGAGCGGACTCTGGAGCAGCTCTTGGAGATTCA--G 1021
QY 616 GGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGATCAAGGGATCCTGGCA 675

GENERAL INFORMATION:
 APPLICANT: Solimena, Michele
 TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
 TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
 FILE REFERENCE: 101918-200 (OCR-941)
 CURRENT APPLICATION NUMBER: US/09/368,590
 CURRENT FILING DATE: 1999-08-04
 EARLIER APPLICATION NUMBER: 60/095,657
 EARLIER FILING DATE: 1998-08-07
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1

LENGTH: 7812

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(6879)

NAME/KEY: unsure

LOCATION: (100)...(102)

NAME/KEY: unsure

LOCATION: (1021)...(1023)

NAME/KEY: unsure

LOCATION: (2266)...(2268)

US-09-368-590-1

Query Match 2.9%; Score 42.8; DB 3; Length 7812;
 Best Local Similarity 47.9%; Pred. No. 0.0071;
 Matches 156; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

QY	601	CCAGGAACCTCAAGAGCCGACGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT	660
Db	3639	CAAGGAGTTGCACACAGGTGGCGCAGCACCTGGACGACGCTGGCATGGTTTCAGGAGCG	3698
QY	661	CAAGGGA---TCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCT	717
Db	3699	GCTGCCACTGGCCATGCAGACAGAGCGAGGCAACGGTTTGCAGCGGTTCCAGCAGCACAT	3758
QY	718	CGAGAAAGTCAAGGCACTTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTTGAGCCACGT	777
Db	3759	CAAAAGAACCCAGGGCCTGCGCGGGAGATCCAGGCGCATGGCGCGCTGGAGGAGGT	3818
QY	778	CAATGACCTTGCTGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCGTATACCTCAG	837
Db	3819	GCTGGAGCGCGGGCGCGTGGCGGTGCTGCGCAGCCCGGAGGAGGAGGAGTGGCGCG	3878
QY	838	CACCTTGAAGACCTGAACACAGATGGAAGCTTCTGAGGTTGGCGGTGCGGAGACCGAGT	897
Db	3879	GGCGCTGGAGCAGCTGCAGAGCGCTGGCGGAGTGGCGGAGGCTGCCGAGCGACGGCA	3938
QY	898	CAGGAGCTGCATGAAGCCACAGGG	923
Db	3939	GCAGTGTGGACGCGCGCTTCCAGG	3964

RESULT 13

US-08-425-069-3

Sequence 3, Application US/08425069

Patent No. 5728810

GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V.

APPLICANT: Xu, Ming

APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: 301 No. 5728810th Washington Street

CITY: Falls Church

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22046
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/425,069
 FILING DATE: 19-APR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1447-106P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1995 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 IMMEDIATE SOURCE:
 CLONE: p6B
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1785
 US-08-425-069-3

Query Match 2.6%; Score 38.6; DB 1; Length 1995;
 Best Local Similarity 44.0%; Pred. No. 0.067;
 Matches 164; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY	311	GCAGTTCAGAACGACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAACTAAAGAA	370
Db	731	GCAGTGCAGCTGCAGCAGCCGCGCAGGACCTGGACAAACAGGACCCGCGGATATGGAC	790
QY	371	CCTGTAATCATGACTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA	430
Db	791	CAGGACAAACAGGACCATCTGGACCCCGTAGTGTCCCTGACGAGCAGCCCGCGCAGCAG	850
QY	431	GGACTAGAGAACTCTACAGGAGCCCGCAGAGAGTCCCTCTGAGGAGAGAGCCCAAGAT	490
Db	851	GACTGGAGGATATGGCCCTGGACAAACAGGACCCGCGGAGGATATGGACCAGGACAAAG	910
QY	491	GTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATCTAGTGGGAAAAATTGAAC	550
Db	911	GACCATCTGGAGCAGGAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGAT	970
QY	551	CTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGAGACTCCAGGAAC	610
Db	971	TAGGAGGTTATGGACCAAGGACCAAGGTTCCAGGAGGATATGGACCAGGACCAAGGTC	1030
QY	611	CAAGAGGCCACGGATGAGTGGACCTCAAGCTGGCCCAAGCTGAGGTGATCAAGGGATCC	670
Db	1031	CAGGAGGATATGGACCAAGGTTAGTGTCTGACAGCAGCAGCCGCGCAGGACCTGGACAAC	1090
QY	671	TGGCAGCCCGTGG	683
Db	1091	AAGGACCAGGAGG	1103

RESULT 14

US-08-317-844B-3

Sequence 3, Application US/08317844B

Patent No. 5989894

GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V.

APPLICANT: Xu, Ming

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Perfect score: 1501
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1501	100.0	3858	10	US-09-845-416-9
4	1501	100.0	3999	10	US-09-845-416-6
5	1501	100.0	4182	10	US-09-845-416-2
6	1501	100.0	4498	10	US-09-845-416-30
7	1501	100.0	4825	10	US-09-845-416-29
8	1501	100.0	4848	10	US-09-845-416-35
9	1501	100.0	4966	10	US-09-845-416-28
10	1501	100.0	4990	10	US-09-845-416-34
11	1501	100.0	5060	10	US-09-845-416-36
12	1501	100.0	5149	10	US-09-845-416-27
13	1501	100.0	5339	16	US-10-149-736-40
14	1501	100.0	5462	16	US-10-149-736-41

15	1501	100.0	8689	16	US-10-149-736-42	Sequence 42, Appl
16	1501	100.0	11058	10	US-09-845-416-1	Sequence 1, Appli
17	1501	100.0	11443	16	US-10-149-736-44	Sequence 44, Appl
18	1501	100.0	12057	16	US-10-149-736-47	Sequence 47, Appl
19	1501	100.0	13957	9	US-09-782-378A-22	Sequence 22, Appl
20	1501	100.0	13957	9	US-09-880-107-2284	Sequence 2284, Ap
21	1501	100.0	13957	16	US-10-149-736-1	Sequence 1, Appli
22	1501	100.0	14069	13	US-10-342-887-434	Sequence 434, App
23	1501	100.0	14069	13	US-10-172-118-434	Sequence 434, App
24	1501	100.0	14082	13	US-10-342-887-981	Sequence 981, App
25	1501	100.0	14082	13	US-10-172-118-981	Sequence 981, App
26	1501	100.0	14082	16	US-10-341-434-108	Sequence 108, App
27	1307.8	87.1	3510	10	US-09-845-416-12	Sequence 12, Appl
28	1307.8	87.1	4476	10	US-09-845-416-31	Sequence 31, Appl
29	1303	86.8	1821	10	US-09-845-416-13	Sequence 13, Appl
30	1298.4	86.5	13815	16	US-10-149-736-2	Sequence 2, Appli
31	917.6	61.1	3446	10	US-09-845-416-14	Sequence 14, Appl
32	917.6	61.1	4414	10	US-09-845-416-32	Sequence 32, Appl
33	916.6	61.1	5417	16	US-10-149-736-39	Sequence 39, Appl
34	916	61.0	1434	10	US-09-845-416-15	Sequence 15, Appl
35	619.2	41.3	10705	12	US-10-152-319A-1598	Sequence 1598, Ap
36	619.2	41.3	11096	16	US-10-149-736-4	Sequence 4, Appli
37	604.8	40.3	10302	9	US-09-782-378A-23	Sequence 23, Appl
38	604.8	40.3	10302	16	US-10-149-736-3	Sequence 3, Appli
39	596	39.7	16531	15	US-10-101-510-667	Sequence 667, App
40	534	35.6	5106	13	US-10-220-120-157	Sequence 157, App
41	387	25.8	387	16	US-10-149-736-32	Sequence 32, Appl
42	372	24.8	887	16	US-10-149-736-35	Sequence 35, Appl
43	324	21.6	324	16	US-10-149-736-33	Sequence 33, Appl
44	216	14.4	216	16	US-10-149-736-34	Sequence 34, Appl
45	202	13.5	348	16	US-10-149-736-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-845-416-4
; Sequence 4, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-4

Query Match 100.0%; Score 1501; DB 10; Length 2169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACAATGGCAAGACCTCCAAGGTGAAATTGAAGTCAACAGATGTTTATCACAACCTGGA	60
Db	151	ACAATGGCAAGACCTCCAAGGTGAAATTGAAGTCAACAGATGTTTATCACAACCTGGA	210
Qy	61	TGAAAAACAGCCAAAAATCCTGAGATCCCTGGAGGTTCCGATGATGCAGTCTGTTACA	120
Db	211	TGAAAAACAGCCAAAAATCCTGAGATCCCTGGAGGTTCCGATGATGCAGTCTGTTACA	270
Qy	121	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGAAAAAGTCTCTCAACAT	180
Db	271	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGAAAAAGTCTCTCAACAT	330

QY 181 TAGGTCCCATTTGGAAAGCCAGTTCTGACAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 331 TAGGTCCCATTTGGAAAGCCAGTTCTGACAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 390
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGAGGCACCTATTGGAGG 300
Db 391 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGAGGCACCTATTGGAGG 450
QY 301 CGACTTTCCAGAGTTTCAAGAGCAGAACGATGTACATAGGSCCTTCAAGAGGGAATTGAA 360
Db 451 CGACTTTCCAGAGTTTCAAGAGCAGAACGATGTACATAGGSCCTTCAAGAGGGAATTGAA 510
QY 361 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGCAGAGCA 420
Db 511 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGCAGAGCA 570
QY 421 GCCTTTTGGAGGACTAGAGAACTCTACAGAGAGCCAGAGAGCTGCCTCCTGAGGAGAG 480
Db 571 GCCTTTTGGAGGACTAGAGAACTCTACAGAGAGCCAGAGAGCTGCCTCCTGAGGAGAG 630
QY 481 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 540
Db 631 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 690
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 600
Db 691 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 750
QY 601 CCAGGAACCTCAAGAGGCCACCGATGAGCTGAGACCTCAAGCTGCGCCAAGCTGAGGTGAT 660
Db 751 CCAGGAACCTCAAGAGGCCACCGATGAGCTGAGACCTCAAGCTGCGCCAAGCTGAGGTGAT 810
QY 661 CAAGGATTCCTGGCAGCCCGTGGCGCATCTCCTCATTCATCTCTCCAAGATCACCTCGA 720
Db 811 CAAGGATTCCTGGCAGCCCGTGGCGCATCTCCTCATTCATCTCTCCAAGATCACCTCGA 870
QY 721 GAAAGTCAAGGCACCTTCAGGAGAGAAATTCGCGCTCTGAAAGAGAACGCTGAGCCACGTCAA 780
Db 871 GAAAGTCAAGGCACCTTCAGGAGAGAAATTCGCGCTCTGAAAGAGAACGCTGAGCCACGTCAA 930
QY 781 TGACCTTGCTCGCCAGCTTACCCTTTGGGCATTCAGCTCTCACCGTATACCTCAGCAC 840
Db 931 TGACCTTGCTCGCCAGCTTACCCTTTGGGCATTCAGCTCTCACCGTATACCTCAGCAC 990
QY 841 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAAGTGGCCGTCGAGGACCGAGTCAG 900
Db 991 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAAGTGGCCGTCGAGGACCGAGTCAG 1050
QY 901 GCAGCTGCATGAAGCCACAGGSACTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC 960
Db 1051 GCAGCTGCATGAAGCCACAGGSACTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTC 1110
QY 961 TGTCCAGGCTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCA 1020
Db 1111 TGTCCAGGCTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCA 1170
QY 1021 CGAGACTCAACAACTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAAGTCTTTAGC 1080
Db 1171 CGAGACTCAACAACTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAAGTCTTTAGC 1230
QY 1081 TGACCTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 1231 TGACCTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1290
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGATGCTGATGCTTGGACCCAGCA 1200
Db 1291 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGATGCTGATGCTTGGACCCAGCA 1350
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCTGCAGATTTAATGTTTGGACCCAC 1260
Db 1351 CAACCTCAAGCAAAATGACAGCCCATGGATATCTGCAGATTTAATGTTTGGACCCAC 1410
QY 1261 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGGA 1320

Db 1411 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGGA 1470
QY 1321 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGCGGACGAAACAGGAGGATCCGTGT 1380
Db 1471 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGCGGACGAAACAGGAGGATCCGTGT 1530
QY 1381 CCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAG 1440
Db 1531 CCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAG 1590
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCT 1500
Db 1591 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCT 1650
QY 1501 C 1501
Db 1651 C 1651

RESULT 2
US-09-845-416-10
; Sequence 10, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-10

Query Match 100.0%; Score 1501; DB 10; Length 3531;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAAGGTGAAATTAAGCTCACACAGATGTTTATCAACAACCTGGA 60
Db 1500 ACAATGGCAAGACCTCCAAAGGTGAAATTAAGCTCACACAGATGTTTATCAACAACCTGGA 1559
QY 61 TGAACAACAGCCAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCGTCTGTATCA 120
Db 1560 TGAACAACAGCCAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCGTCTGTATCA 1619
QY 121 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT 180
Db 1620 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT 1679
QY 181 TAGTCCCATTGGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 1680 TAGTCCCATTGGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 1739
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGAGGCACCTATTGGAGG 300
Db 1740 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGAGGCACCTATTGGAGG 1799
QY 301 CGACTTTCCAGCAGTTTCAAGAGCAGAACCGATGTACATAGGSCCTTCAAGAGGGAATTGAA 360
Db 1800 CGACTTTCCAGCAGTTTCAAGAGCAGAACCGATGTACATAGGSCCTTCAAGAGGGAATTGAA 1859
QY 361 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGCAGAGCA 420
Db 1860 AACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGCAGAGCA 1919

QY 421 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 480
|
Db 1920 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 1979

QY 481 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGAGGTCATACTAGTGGGA 540
|
Db 1980 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGAGGTCATACTAGTGGGA 2039

QY 541 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCTTGAAGACT 600
|
Db 2040 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCTTGAAGACT 2099

QY 601 CCAGGAACCTCAAGAGGCCACGGATGAGCTTGACCTCAAGCTGCGCCAAAGCTGAGTGAT 660
|
Db 2100 CCAGGAACCTCAAGAGGCCACGGATGAGCTTGACCTCAAGCTGCGCCAAAGCTGAGTGAT 2159

QY 661 CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
|
Db 2160 CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 2219

QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTGCGCTCTGAAAGAGAAGCTGAGCCACGTCAA 780
|
Db 2220 GAAAGTCAAGGCACCTTCGAGGAGAAATTGCGCTCTGAAAGAGAAGCTGAGCCACGTCAA 2279

QY 781 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCAC 840
|
Db 2280 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCAC 2339

QY 841 TCTGGAAGACCTGAACACCAGATGGAAGTTTCTGCAGGTGGCGCTCGAGGACCGAGTCAG 900
|
Db 2340 TCTGGAAGACCTGAACACCAGATGGAAGTTTCTGCAGGTGGCGCTCGAGGACCGAGTCAG 2399

QY 901 GCAGCTGCATGAAGCCCCACAGGGACTTTGGTCCAGCATCTCAGGACTTTCTTTCCACGTC 960
|
Db 2400 GCAGCTGCATGAAGCCCCACAGGGACTTTGGTCCAGCATCTCAGGACTTTCTTTCCACGTC 2459

QY 961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA 1020
|
Db 2460 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA 2519

QY 1021 CGAGACTCAAAACACTTGCTGGGACCAATCCCAAAATGACAGAGCTCTACAGTCTTTAGC 1080
|
Db 2520 CGAGACTCAAAACACTTGCTGGGACCAATCCCAAAATGACAGAGCTCTACAGTCTTTAGC 2579

QY 1081 TGACCTGAATATGTCCAGATTCTCAGCTTATAGGACTGCCATGAACCTCCGAAGACTGCA 1140
|
Db 2580 TGACCTGAATATGTCCAGATTCTCAGCTTATAGGACTGCCATGAACCTCCGAAGACTGCA 2639

QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCAATGTGATGCTTGGACCAAGCA 1200
|
Db 2640 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCAATGTGATGCTTGGACCAAGCA 2699

QY 1201 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCCAC 1260
|
Db 2700 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCCAC 2759

QY 1261 TATTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA 1320
|
Db 2760 TATTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA 2819

QY 1321 TATGTGTCTGAACCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380
|
Db 2820 TATGTGTCTGAACCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 2879

QY 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAG 1440
|
Db 2880 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAG 2939

QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT 1500
|
Db 2940 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT 2999

QY 1501 C 1501

Db 3000 C 3000

RESULT 3

US-09-845-416-9
; Sequence 9, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-9

Query Match 100.0%; Score 1501; DB 10; Length 3858;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGA 60
|
Db 1827 ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGA 1886

QY 61 TGAACACAGCCAAATAATCCTGAGATCCCTGGAAGTTCOGATGATGCAGTCTCTTACA 120
|
Db 1887 TGAACACAGCCAAATAATCCTGAGATCCCTGGAAGTTCOGATGATGCAGTCTCTTACA 1946

QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTCGGAAAAAGTCTCTCAACAT 180
|
Db 1947 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTCGGAAAAAGTCTCTCAACAT 2006

QY 181 TAGTCCCATTGGAAGCCAGTTCTGACAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 240
|
Db 2007 TAGTCCCATTGGAAGCCAGTTCTGACAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 2066

QY 241 ACTTCTGGTGTGGTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG 300
|
Db 2067 ACTTCTGGTGTGGTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG 2126

QY 301 CGACTTTCCAGCAGTTCAAGAAAGCAGAACCGATGACATAGGCGCTTCAAGAGGGGAATTGAA 360
|
Db 2127 CGACTTTCCAGCAGTTCAAGAAAGCAGAACCGATGACATAGGCGCTTCAAGAGGGGAATTGAA 2186

QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA 420
|
Db 2187 AACTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA 2246

QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACCAGAGCCCCAGAGAGCTGCCTCCTGAGGAGAG 480
|
Db 2247 GCCTTTGGAAGGACTAGAGAAACTCTACCAGAGCCCCAGAGAGCTGCCTCCTGAGGAGAG 2306

QY 481 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
|
Db 2307 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 2366

QY 541 AAAATTGAACCTGCATCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 600
|
Db 2367 AAAATTGAACCTGCATCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 2426

QY 601 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGAACCTCAAGCTGCGCCAAAGCTGAGGTGAT 660
|
Db 2427 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGAACCTCAAGCTGCGCCAAAGCTGAGGTGAT 2486

QY 661 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTATTGACTCTCTCCAAGATCACCTCGA 720
Db |||||
QY 2487 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTATTGACTCTCTCCAAGATCACCTCGA 2546
Db |||||
QY 721 GAAAGTCAAGGCACTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGTCGAGCCACGTCAA 780
Db |||||
QY 2547 GAAAGTCAAGGCACTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGTCGAGCCACGTCAA 2606
Db |||||
QY 781 TGACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAAACCCTCAGC 840
Db |||||
QY 2607 TGACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAAACCCTCAGC 2666
Db |||||
QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG 900
Db |||||
QY 2667 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG 2726
Db |||||
QY 901 GCAGCTGATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACTTCTTCTTCCAGCTC 960
Db |||||
QY 2727 GCAGCTGATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACTTCTTCTTCCAGCTC 2786
Db |||||
QY 961 TGTCCAGGTCCTGGGAGAGAGGACCTCTCGCCCAACAAAGTGCCTACTATATCAACCA 1020
Db |||||
QY 2787 TGTCCAGGTCCTGGGAGAGAGGACCTCTCGCCCAACAAAGTGCCTACTATATCAACCA 2846
Db |||||
QY 1021 CGAGACTCAACAACTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db |||||
QY 2847 CGAGACTCAACAACTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 2906
Db |||||
QY 1081 TGACCTGAATAATGTGATCTCAGCTTATAGGACTGACATGAACTCCGAGACTGCA 1140
Db |||||
QY 2907 TGACCTGAATAATGTGATCTCAGCTTATAGGACTGACATGAACTCCGAGACTGCA 2966
Db |||||
QY 1141 GAAGGCCCTTGTCTGGATCTCTGAGCCTGTGATGATGATGATGATGATGATGATGATGAT 1200
Db |||||
QY 2967 GAAGGCCCTTGTCTGGATCTCTGAGCCTGTGATGATGATGATGATGATGATGATGATGAT 3026
Db |||||
QY 1201 CAACCTCAAGCAAAATGACCCAGCCATGGATATCCTGCAGATTAATTAATTTGTTGACCA 1260
Db |||||
QY 3027 CAACCTCAAGCAAAATGACCCAGCCATGGATATCCTGCAGATTAATTAATTTGTTGACCA 3086
Db |||||
QY 1261 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGTTCAACGTCCCTCTCTGCGTGA 1320
Db |||||
QY 3087 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGTTCAACGTCCCTCTCTGCGTGA 3146
Db |||||
QY 1321 TATGTGTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380
Db |||||
QY 3147 TATGTGTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 3206
Db |||||
QY 1381 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1440
Db |||||
QY 3207 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 3266
Db |||||
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCGAGCGGCTGGGCCT 1500
Db |||||
QY 3267 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCGAGCGGCTGGGCCT 3326
Db |||||
QY 1501 C 1501
Db 3327 C 3327

RESULT 4
US-09-845-416-6
; Sequence 6, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777

; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-6

Query Match 100.0%; Score 1501; DB 10; Length 3999;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAGGTGAAATTTGAAGCTCACACAGATGTTTATCACAACCTGGA 60
Db |||||
QY 1968 ACAATGGCAAGACCTCCAAGGTGAAATTTGAAGCTCACACAGATGTTTATCACAACCTGGA 2027
Db |||||
QY 61 TGAACACAGCCAAATAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCCCTGTACA 120
Db |||||
QY 2028 TGAACACAGCCAAATAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCCCTGTACA 2087
Db |||||
QY 121 AAGACGTTTGGATAACATGAATCAAGTGGAGTGAAGTTCGGAAGAAAGTCTCTCAACAT 180
Db |||||
QY 2088 AAGACGTTTGGATAACATGAATCAAGTGGAGTGAAGTTCGGAAGAAAGTCTCTCAACAT 2147
Db |||||
QY 181 TAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCCGTCTGCACCTTTCTCTGCAGGA 240
Db |||||
QY 2148 TAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCCGTCTGCACCTTTCTCTGCAGGA 2207
Db |||||
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db |||||
QY 2208 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 2267
Db |||||
QY 301 CGACTTCCAGCAGTTTCAGAACAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 360
Db |||||
QY 2268 CGACTTCCAGCAGTTTCAGAACAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 2327
Db |||||
QY 361 AACTAAAGAACCTGTATATCATGAGTACTCTTCCAGGAGCCACAGAGAGCTGCCTCCTCAGGAG 420
Db |||||
QY 2328 AACTAAAGAACCTGTATATCATGAGTACTCTTCCAGGAGCCACAGAGAGCTGCCTCCTCAGGAG 2387
Db |||||
QY 421 GCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCACAGAGAGCTGCCTCCTCAGGAGAG 480
Db |||||
QY 2388 GCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCACAGAGAGCTGCCTCCTCAGGAGAG 2447
Db |||||
QY 481 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATATCTGAGTGGGA 540
Db |||||
QY 2448 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATATCTGAGTGGGA 2507
Db |||||
QY 541 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTGAAGACT 600
Db |||||
QY 2508 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTGAAGACT 2567
Db |||||
QY 601 CCAGGAACCTTCAAGAGGCGCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 660
Db |||||
QY 2568 CCAGGAACCTTCAAGAGGCGCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 2627
Db |||||
QY 661 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
Db |||||
QY 2628 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 2687
Db |||||
QY 721 GAAAGTCAAGGCACTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGTCGAGCCACGTCAA 780
Db |||||
QY 2688 GAAAGTCAAGGCACTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGTCGAGCCACGTCAA 2747
Db |||||
QY 781 TGACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAAACCCTCAGCAC 840
Db |||||
QY 2748 TGACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAAACCCTCAGCAC 2807
Db |||||
QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAG 900
Db |||||
QY 2808 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAG 2867
Db |||||

QY 901 GCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 960
Db 2868 GCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 2927
QY 961 TGTCCAGGTCCTTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020
Db 2928 TGTCCAGGTCCTTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 2987
QY 1021 CGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGC 1080
Db 2988 CGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGC 3047
QY 1081 TGACCTGAATAATGTCAGATTCTCTAGCCCTCTCAGCTGCATGTGATGCTTTAGC 1140
Db 3048 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA 3107
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTCTCAGCTGCATGTGATGCTTTAGC 1200
Db 3108 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTCTCAGCTGCATGTGATGCTTTAGC 3167
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCA 1260
Db 3168 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCA 3227
QY 1261 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
Db 3228 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 3287
QY 1321 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1380
Db 3288 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 3347
QY 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAATACAG 1440
Db 3348 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAATACAG 3407
QY 1441 ATACCTTTTCAAGCAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGCCT 1500
Db 3408 ATACCTTTTCAAGCAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGCCT 3467
QY 1501 C 1501
Db 3468 C 3468

RESULT 5
US-09-845-416-2
; Sequence 2, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-2

Query Match 100.0%; Score 1501; DB 10; Length 4182;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAGGTGAAATTGAAGCTCACACAGATGTTTATCAACACCTGGA 60
Db 2151 ACAATGGCAAGACCTCCAGGTGAAATTGAAGCTCACACAGATGTTTATCAACACCTGGA 2210

QY 61 TGAAAAACAGCCAAAAAATCCTGAGATCCCTGGAAAGGTTCCGATGATGCACTCCTGTTACA 120
Db 2211 TGAAAAACAGCCAAAAAATCCTGAGATCCCTGGAAAGGTTCCGATGATGCACTCCTGTTACA 2270
QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 180
Db 2271 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT 2330
QY 181 TAGGTCCCATTTGGAAAGCCAGTTTCTGACCACTGGAAAGCGTCTGCACCTTCTCTGACAGGA 240
Db 2331 TAGGTCCCATTTGGAAAGCCAGTTTCTGACCACTGGAAAGCGTCTGCACCTTCTCTGACAGGA 2390
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGCACTATTGGAGG 300
Db 2391 ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGCACTATTGGAGG 2450
QY 301 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGGAATTGAA 360
Db 2451 CGACTTTCCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGGAATTGAA 2510
QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db 2511 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 2570
QY 421 GCCTTTTGAAGGACTAGAGAAACTCTACCAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 480
Db 2571 GCCTTTTGAAGGACTAGAGAAACTCTACCAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 2630
QY 481 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACCTGAGTGGGA 540
Db 2631 AGCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACCTGAGTGGGA 2690
QY 541 AAAATTGAACCTGCATCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 600
Db 2691 AAAATTGAACCTGCATCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT 2750
QY 601 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGAT 660
Db 2751 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGAT 2810
QY 661 CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
Db 2811 CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 2870
QY 721 GAAAGTCAAGGCACCTTCGAGAGAAAAATTGCGCCTCTGAAAAGAGAACGTGAGCCACGTCAA 780
Db 2871 GAAAGTCAAGGCACCTTCGAGAGAAAAATTGCGCCTCTGAAAAGAGAACGTGAGCCACGTCAA 2930
QY 781 TGACCTTGTCTGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 840
Db 2931 TGACCTTGTCTGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 2990
QY 841 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAAGTGGCCGTGAGGACCGAGTCAAG 900
Db 2991 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAAGTGGCCGTGAGGACCGAGTCAAG 3050
QY 901 GCAGCTGCATGAAGCCCAAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 960
Db 3051 GCAGCTGCATGAAGCCCAAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 3110
QY 961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCCAAAAGTGGCCCTACTATATCAACCA 1020
Db 3111 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCCAAAAGTGGCCCTACTATATCAACCA 3170
QY 1021 CGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db 3171 CGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 3230
QY 1081 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA 1140
Db 3231 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA 3290

QY 1141 GAAGGCCCTTTGGTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCCTTGGACCAGCA 1200
| | | | |
Db 3291 GAAGGCCCTTTGGTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCCTTGGACCAGCA 3350
| | | | |
QY 1201 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 1260
| | | | |
Db 3351 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 3410
| | | | |
QY 1261 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA 1320
| | | | |
Db 3411 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA 3470
| | | | |
QY 1321 TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380
| | | | |
Db 3471 TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 3530
| | | | |
QY 1381 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAG 1440
| | | | |
Db 3531 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAG 3590
| | | | |
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCT 1500
| | | | |
Db 3591 ATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCT 3650
| | | | |
QY 1501 C 1501
| | | | |
Db 3651 C 3651
| | | | |

RESULT 6
US-09-845-416-30
; Sequence 30, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-30

Query Match 100.0%; Score 1501; DB 10; Length 4498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAGGTGAATTTGAAGCTCACACAGATGTTTATCAACAACCTGGA 60
| | | | |
Db 2257 ACAATGGCAAGACCTCCAAGGTGAATTTGAAGCTCACACAGATGTTTATCAACAACCTGGA 2316
| | | | |
QY 61 TGAACAAGCCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCGTGTACA 120
| | | | |
Db 2317 TGAACAAGCCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCGTGTACA 2376
| | | | |
QY 121 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTCGGAAAAAGTCTCTCAACAT 180
| | | | |
Db 2377 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTCGGAAAAAGTCTCTCAACAT 2436
| | | | |
QY 181 TAGGTCCCATTTGGAAGCCAGTCTTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 240
| | | | |
Db 2437 TAGGTCCCATTTGGAAGCCAGTCTTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 2496
| | | | |
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
| | | | |
Db 2497 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 2556
| | | | |

QY 301 CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 360
| | | | |
Db 2557 CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 2616
| | | | |
QY 361 AACTAAAGAACTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
| | | | |
Db 2617 AACTAAAGAACTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 2676
| | | | |
QY 421 GCCTTTTGGAGGACTAGAGAAACTCTACCAAGGAGGCCCCAGAGAGCTGCCTCCTGAGGAGAG 480
| | | | |
Db 2677 GCCTTTTGGAGGACTAGAGAAACTCTACCAAGGAGGCCCCAGAGAGCTGCCTCCTGAGGAGAG 2736
| | | | |
QY 481 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
| | | | |
Db 2737 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 2796
| | | | |
QY 541 AAAATTGAACCTGCACCTCGCTGTACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 600
| | | | |
Db 2797 AAAATTGAACCTGCACCTCGCTGTACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 2856
| | | | |
QY 601 CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 660
| | | | |
Db 2857 CCAGGAACCTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 2916
| | | | |
QY 661 CAAGGGATCTTGGCAGCCCGTGGCGGATCTCTCAATTGACTCTCTCCAAGATCACTCGA 720
| | | | |
Db 2917 CAAGGGATCTTGGCAGCCCGTGGCGGATCTCTCAATTGACTCTCTCCAAGATCACTCGA 2976
| | | | |
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCAA 780
| | | | |
Db 2977 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCAA 3036
| | | | |
QY 781 TGACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 840
| | | | |
Db 3037 TGACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 3096
| | | | |
QY 841 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGTGGCCGTGAGGACCCGAGTCAG 900
| | | | |
Db 3097 TCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCAGTGGCCGTGAGGACCCGAGTCAG 3156
| | | | |
QY 901 GCAGCTGCATGAAGCCCAAGGACCTTTGGTCCAGCATCTCAGCAGCTTCTTCTCCACGTC 960
| | | | |
Db 3157 GCAGCTGCATGAAGCCCAAGGACCTTTGGTCCAGCATCTCAGCAGCTTCTTCTCCACGTC 3216
| | | | |
QY 961 TGTCAGGCTCCCTGGGAGAGAGCCCATCTCGCCCAAAAGTGCCTACTATATCAACCA 1020
| | | | |
Db 3217 TGTCAGGCTCCCTGGGAGAGAGCCCATCTCGCCCAAAAGTGCCTACTATATCAACCA 3276
| | | | |
QY 1021 CGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
| | | | |
Db 3277 CGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 3336
| | | | |
QY 1081 TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAGAGACTGCA 1140
| | | | |
Db 3337 TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAGAGACTGCA 3396
| | | | |
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCA 1200
| | | | |
Db 3397 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCA 3456
| | | | |
QY 1201 CAACCTCAAGCAAAAATGACAGCCCATGGATATCTTCAGAGATTATTAATTGTTGACCCAG 1260
| | | | |
Db 3457 CAACCTCAAGCAAAAATGACAGCCCATGGATATCTTCAGAGATTATTAATTGTTGACCCAG 3516
| | | | |
QY 1261 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA 1320
| | | | |
Db 3517 TATTTATGACCCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGA 3576
| | | | |
QY 1321 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380
| | | | |
Db 3577 TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 3636
| | | | |

QY	1381	CCTGTCCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAAGACAAGTACAG	1440
Db	3637	CCTGTCCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAAGACAAGTACAG	3696
QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGCTGGGCCT	1500
Db	3697	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGCTGGGCCT	3756
QY	1501	C 1501	
Db	3757	C 3757	

RESULT 7

US-09-845-416-29

; Sequence 29, Application US/09845416

; Publication No. US20030171312A1

; GENERAL INFORMATION:

; APPLICANT: XIAO, XIAO

; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: DE1142

; CURRENT APPLICATION NUMBER: US/09/845,416

; CURRENT FILING DATE: 2001-04-30

; PRIOR APPLICATION NUMBER: 60/200,777

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 29

; LENGTH: 4825

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-845-416-29

RESULT 8
US-09-845-416-35
: Sequence 35. Application US/09845416

Publication No. US20030171312A1
GENERAL INFORMATION:
APPLICANT: XIAO, XIAO
TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
FILE REFERENCE: DE1142
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,777
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 4848
TYPE: DNA
ORGANISM: Homo sapiens
US-09-845-416-35

Query Match 100.0%; Score 1501; DB 10; Length 4848;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAGGTGAATGAAGTCAACAGCTCACACAGATGTTTATCAACAACCTGGA 60
Db 2607 ACAATGGCAAGACCTCCAAGGTGAATGAAGTCAACAGCTCACACAGATGTTTATCAACAACCTGGA 2666

QY 61 TGAACAACAGCCAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 120
Db 2667 TGAACAACAGCCAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 2726

QY 121 AAGACGTTTGGATAAATCAAGTCAAGTGAAGTGAACCTCGGAAAAAGTCTCTCAACAT 180
Db 2727 AAGACGTTTGGATAAATCAAGTCAAGTGAAGTGAACCTCGGAAAAAGTCTCTCAACAT 2786

QY 181 TAGGTCCCAATTTGGAAGCCAGTTCTGACAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 2787 TAGGTCCCAATTTGGAAGCCAGTTCTGACAGTGAAGCGTCTGCACCTTTCTCTGCAGGA 2846

QY 241 ACTTCTGTTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db 2847 ACTTCTGTTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 2906

QY 301 CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAA 360
Db 2907 CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAA 2966

QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCA 420
Db 2967 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCA 3026

QY 421 GCCTTTGGAAGGACTAGAGAACTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 480
Db 3027 GCCTTTGGAAGGACTAGAGAACTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 3086

QY 481 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db 3087 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 3146

QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAATAGATGAGACCCCTTGAAGACT 600
Db 3147 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAATAGATGAGACCCCTTGAAGACT 3206

QY 601 CCAGGAATCTCAAGAGGCCACGATGAGTGGACCTCAAGCTGCGCAAGCTGAGGTGAT 660
Db 3207 CCAGGAATCTCAAGAGGCCACGATGAGTGGACCTCAAGCTGCGCAAGCTGAGGTGAT 3266

QY 661 CAAGGATCCTGGCAGCCCGTGGCGGATCTCTCAATGACTCTCTCCAAGATCACCTCGA 720
Db 3267 CAAGGATCCTGGCAGCCCGTGGCGGATCTCTCAATGACTCTCTCCAAGATCACCTCGA 3326

QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGTCGAGCCAGTCAA 780
Db 3327 GAAAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGTCGAGCCAGTCAA 3386

QY 781 TGACCTTGTCTGCCAGCTTACCACTTTGGGCATTACAGCTCTACCCGTATAACCTCAGCAC 840
Db 3387 TGACCTTGTCTGCCAGCTTACCACTTTGGGCATTACAGCTCTACCCGTATAACCTCAGCAC 3446

QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCGCTCGAGGACCGAGTCAG 900
Db 3447 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCGCTCGAGGACCGAGTCAG 3506

QY 901 GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGCACTTCTTCCAGTC 960
Db 3507 GCAGCTGCATGAAGCCACACAGGACTTTGGTCCAGCATCTCAGCACTTCTTCCAGTC 3566

QY 961 TGTCCAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020
Db 3567 TGTCCAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 3626

QY 1021 CGAGACTCAAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTTACCAGTCTTTAGC 1080
Db 3627 CGAGACTCAAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTTACCAGTCTTTAGC 3686

QY 1081 TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 3687 TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 3746

QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGATGTCCTTTGGACCAGCA 1200
Db 3747 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGATGTCCTTTGGACCAGCA 3806

QY 1201 CAACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGACAGATTATTAATGTTTGACCAC 1260
Db 3807 CAACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGACAGATTATTAATGTTTGACCAC 3866

QY 1261 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGCTCCCTCTCTGCGTGA 1320
Db 3867 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGCTCCCTCTCTGCGTGA 3926

QY 1321 TATGTGTCTGAACCTGGCTGTGTAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1380
Db 3927 TATGTGTCTGAACCTGGCTGTGTAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 3986

QY 1381 CCTGTCTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAGTACAG 1440
Db 3987 CCTGTCTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAGTACAG 4046

QY 1441 ATACCTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCGCAGCGTGGGCT 1500
Db 4047 ATACCTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCGCAGCGTGGGCT 4106

QY 1501 C 1501
Db 4107 C 4107

RESULT 9
US-09-845-416-28
; Sequence 28, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 4966
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-845-416-28									
Query Match 100.0%; Score 1501; DB 10; Length 4966;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ACAATGGCAACCTCCAAAGGTGAATTTGAAGCTCACACAGATGTTTATCAACAACCTTGA	60						
Db	2725	ACAATGGCAACCTCCAAAGGTGAATTTGAAGCTCACACAGATGTTTATCAACAACCTTGA	2784						
QY	61	TGAAAACAGCCAAAAATCCTGAGATCCCTGGAAAGTTCCGATGATGCAGTCTCTGTACA	120						
Db	2785	TGAAAACAGCCAAAAATCCTGAGATCCCTGGAAAGTTCCGATGATGCAGTCTCTGTACA	2844						
QY	121	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT	180						
Db	2845	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACAT	2904						
QY	181	TAGTCCCATTTGGAAGCCAGTTCTTGACAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA	240						
Db	2905	TAGTCCCATTTGGAAGCCAGTTCTTGACAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA	2964						
QY	241	ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG	300						
Db	2965	ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG	3024						
QY	301	CGACTTTCAGCAGTTCAGAAGCAGAACCGATGTACATAGGGCCCTCAAGAGGGAAATTGAA	360						
Db	3025	CGACTTTCAGCAGTTCAGAAGCAGAACCGATGTACATAGGGCCCTCAAGAGGGAAATTGAA	3084						
QY	361	AACTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA	420						
Db	3085	AACTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA	3144						
QY	421	GCCTTTTGGAAAGGACTAGAGAAACTCTACCAGAGCCCGAGAGCTGCTCCTGAGGAGAG	480						
Db	3145	GCCTTTTGGAAAGGACTAGAGAAACTCTACCAGAGCCCGAGAGCTGCTCCTGAGGAGAG	3204						
QY	481	AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA	540						
Db	3205	AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA	3264						
QY	541	AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT	600						
Db	3265	AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT	3324						
QY	601	CCAGGAACTTCAAGAGCCACGGATGAGCTGGACCTCAAGCTGGCCAAAGCTGAGGTGAT	660						
Db	3325	CCAGGAACTTCAAGAGCCACGGATGAGCTGGACCTCAAGCTGGCCAAAGCTGAGGTGAT	3384						
QY	661	CAAGGGATCCTGGAGCCCGTGGCGATCTCTCATTTGACTCTCTCCAAGATCACCTCGA	720						
Db	3385	CAAGGGATCCTGGAGCCCGTGGCGATCTCTCATTTGACTCTCTCCAAGATCACCTCGA	3444						
QY	721	GAAAGTCAAGGCACCTTCGAGGAGAAAATTGGCCCTCTGAAAAGAGAACGTGAGCCACGTCAA	780						
Db	3445	GAAAGTCAAGGCACCTTCGAGGAGAAAATTGGCCCTCTGAAAAGAGAACGTGAGCCACGTCAA	3504						
QY	781	TGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATACCTCAGCAC	840						
Db	3505	TGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATACCTCAGCAC	3564						
QY	841	TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGCTCGAGGACCGAGTCA	900						
Db	3565	TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGCTCGAGGACCGAGTCA	3624						
QY	901	GCAGCTGCATGAAGCCCAAGGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTC	960						
Db	3625	GCAGCTGCATGAAGCCCAAGGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTC	3684						
QY	961	TGTCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCCAACAAAGTGCCTACTATATCAACCA	1020						
Db	3685	TGTCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCCAACAAAGTGCCTACTATATCAACCA	3744						

QY	1021	CGAGACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTTAGC	1080						
Db	3745	CGAGACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTTAGC	3804						
QY	1081	TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA	1140						
Db	3805	TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA	3864						
QY	1141	GAAAGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCTTGGACCAGCA	1200						
Db	3865	GAAAGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCTTGGACCAGCA	3924						
QY	1201	CAACCTCAAGCAAAAATGACAGCCCATGGATATCTCTGCAGATTATTAATTGTTGACCCAC	1260						
Db	3925	CAACCTCAAGCAAAAATGACAGCCCATGGATATCTCTGCAGATTATTAATTGTTGACCCAC	3984						
QY	1261	TATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGA	1320						
Db	3985	TATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGA	4044						
QY	1321	TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT	1380						
Db	4045	TATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT	4104						
QY	1381	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	1440						
Db	4105	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	4164						
QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT	1500						
Db	4165	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT	4224						
QY	1501	C 1501							
Db	4225	C 4225							

RESULT 10

US-09-845-416-34

Sequence 34, Application US/09845416

Publication No. US20030171312A1

GENERAL INFORMATION:

APPLICANT: XIAO, XIAO

TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE

TITLE OF INVENTION: THEREOF

FILE REFERENCE: DE1142

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/200,777

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 34

LENGTH: 4990

TYPE: DNA

ORGANISM: Homo sapiens

US-09-845-416-34

Query Match 100.0%; Score 1501; DB 10; Length 4990;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACAATGGCAAGACCTCCAAAGGTGAAATTTGAAGCTCAACAGATGTTTATCACAACCTTGA	60						
Db	2749	ACAATGGCAAGACCTCCAAAGGTGAAATTTGAAGCTCAACAGATGTTTATCACAACCTTGA	2808						
QY	61	TGAAAACAGCCAAAAATCCTGAGATCCCTGGAAAGTTCCGATGATGCAGTCCCTGTACA	120						
Db	2809	TGAAAACAGCCAAAAATCCTGAGATCCCTGGAAAGTTCCGATGATGCAGTCCCTGTACA	2868						
QY	121	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGAAAAAGTCTCTCAACAT	180						

Db 2869 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT 2928
QY 181 TAGGTCCCATTTTGAAGCCAGTTCTGACCAGTGAAGCGCTCTGCACCTTTCTCTGACGGA 240
Db 2929 TAGGTCCCATTTTGAAGCCAGTTCTGACCAGTGAAGCGCTCTGCACCTTTCTCTGACGGA 2988
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db 2989 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 3048
QY 301 CGACTTTCCAGGAGTTTCAAGAGCAGAACGATGTACATAGGGCTTCAAGAGGGAATTGAA 360
Db 3049 CGACTTTCCAGGAGTTTCAAGAGCAGAACGATGTACATAGGGCTTCAAGAGGGAATTGAA 3108
QY 361 AACTAAAGAACTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCA 420
Db 3109 AACTAAAGAACTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCA 3168
QY 421 GCCTTTTGAAGGACTAGAGAACTCTTACAGAGGAGCCCGAGAGCTGCCTCCTTGAGGAGAG 480
Db 3169 GCCTTTTGAAGGACTAGAGAACTCTTACAGAGGAGCCCGAGAGCTGCCTCCTTGAGGAGAG 3228
QY 481 AGCCCGAATGTCACTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 540
Db 3229 AGCCCGAATGTCACTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 3288
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACT 600
Db 3289 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACT 3348
QY 601 CCAGGAACCTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 660
Db 3349 CCAGGAACCTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 3408
QY 661 CAAGGGATCCTTGGCAGCCCGTGGGCGATCTCCTCATTTGATCTCTCCAAGATCAGCTCGA 720
Db 3409 CAAGGGATCCTTGGCAGCCCGTGGGCGATCTCCTCATTTGATCTCTCCAAGATCAGCTCGA 3468
QY 721 GAAAGTCAAGGCACCTTCGAGGAGGAAATTCGGCTCTGAAAGAGAACGCTGAGCCACGTCAC 780
Db 3469 GAAAGTCAAGGCACCTTCGAGGAGGAAATTCGGCTCTGAAAGAGAACGCTGAGCCACGTCAC 3528
QY 781 TGACCTTGTCTGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATACCTCAGCAC 840
Db 3529 TGACCTTGTCTGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATACCTCAGCAC 3588
QY 841 TCTGGAAGACCTGAAACACCAAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAG 900
Db 3589 TCTGGAAGACCTGAAACACCAAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAG 3648
QY 901 GCAGCTGCATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTC 960
Db 3649 GCAGCTGCATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTC 3708
QY 961 TGTCCAGGTCCTTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 1020
Db 3709 TGTCCAGGTCCTTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 3768
QY 1021 CGAGACTCAAAACAACTTGTGGGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 1080
Db 3769 CGAGACTCAAAACAACTTGTGGGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 3828
QY 1081 TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAGACTGCA 1140
Db 3829 TGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAGACTGCA 3888
QY 1141 GAAGGCCCTTGTCTGGATCTCTTGGCCCTGTGAGCTGCATGTGATGCCCTGACCCAGCA 1200
Db 3889 GAAGGCCCTTGTCTGGATCTCTTGGCCCTGTGAGCTGCATGTGATGCCCTGACCCAGCA 3948
QY 1201 CAACCTCAAGCAAAATGACAGAGCCCATGGATATCCCTGAGATTATTAATTGTTGACCCAC 1260
Db 3949 CAACCTCAAGCAAAATGACAGAGCCCATGGATATCCCTGAGATTATTAATTGTTGACCCAC 4008

RESULT 11

US-09-845-416-36
; Sequence 36, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DB1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 5060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-36

Query Match 100.0%; Score 1501; DB 10; Length 5060;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAAGGTGAAATTTGAAGCTCACACAGATGTTTATCACACCTTGA 60
Db 2819 ACAATGGCAAGACCTCCAAAGGTGAAATTTGAAGCTCACACAGATGTTTATCACACCTTGA 2878
QY 61 TGAAGACAGCCAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 120
Db 2879 TGAAGACAGCCAAATAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCCTGTTACA 2938
QY 121 AAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT 180
Db 2939 AAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT 2998
QY 181 TAGGTCCCATTTTGGAGCCAGTCTTGACCAAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 2999 TAGGTCCCATTTTGGAGCCAGTCTTGACCAAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 3058
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db 3059 ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 3118
QY 301 CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCTTCAAGAGGGAATTGAA 360
Db 3119 CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCTTCAAGAGGGAATTGAA 3178
QY 361 AACTAAAGAACTGTAAATCATGAGTACTCTTGAAGACTGTACGAATATTCTGACAGAGCA 420

Db	3179	AACTAAAGAACTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA	3238
QY	421	GCCTTTGGAAGGACTAGAGAAACTCTACCAAGGAGCCACAGAGAGTGCCCTCCTGAGGAGAG	480
Db	3239	GCCTTTGGAAGGACTAGAGAAACTCTACCAAGGAGCCACAGAGAGTGCCCTCCTGAGGAGAG	3298
QY	481	AGCCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATACTAGTGGGA	540
Db	3299	AGCCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAATACTAGTGGGA	3358
QY	541	AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT	600
Db	3359	AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT	3418
QY	601	CCAGGAACTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGGCCAAAGCTGAGGTGAT	660
Db	3419	CCAGGAACTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGGCCAAAGCTGAGGTGAT	3478
QY	661	CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGA	720
Db	3479	CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGA	3538
QY	721	GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAA	780
Db	3539	GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAA	3598
QY	781	TGACCTTGCTCGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC	840
Db	3599	TGACCTTGCTCGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC	3658
QY	841	TCTGGAAGACCTGAAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG	900
Db	3659	TCTGGAAGACCTGAAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG	3718
QY	901	GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC	960
Db	3719	GCAGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC	3778
QY	961	TGTCCAGGTCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA	1020
Db	3779	TGTCCAGGTCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA	3838
QY	1021	CGAGACTCAAACAACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC	1080
Db	3839	CGAGACTCAAACAACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC	3898
QY	1081	TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA	1140
Db	3899	TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCA	3958
QY	1141	GAAAGCCCTTTGCTTGATCTCTTGAGCCCTGTCAGCTGCATGTGATGCCTTGACCAGCA	1200
Db	3959	GAAAGCCCTTTGCTTGATCTCTTGAGCCCTGTCAGCTGCATGTGATGCCTTGACCAGCA	4018
QY	1201	CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAAATTGTTGACCCAC	1260
Db	4019	CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAAATTGTTGACCCAC	4078
QY	1261	TATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGA	1320
Db	4079	TATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGA	4138
QY	1321	TATGTGCTGAACCTGGTCTGTAATGTTTTATGATACGGGACGAACAGGAGGATCCGTGT	1380
Db	4139	TATGTGCTGAACCTGGTCTGTAATGTTTTATGATACGGGACGAACAGGAGGATCCGTGT	4198
QY	1381	CCTGTCTTTTAAAACTGSCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	1440
Db	4199	CCTGTCTTTTAAAACTGSCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	4258
QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT	1500
Db	4259	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT	4318
QY	1501	C	1501
Db	4319	C	4319
RESULT 12			
US-09-845-416-27			
; Sequence 27, Application US/09845416			
; Publication No. US20030171312A1			
; GENERAL INFORMATION:			
; APPLICANT: XIAO, XIAO			
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: DE1142			
; CURRENT APPLICATION NUMBER: US/09/845,416			
; CURRENT FILING DATE: 2001-04-30			
; PRIOR APPLICATION NUMBER: 60/200,777			
; PRIOR FILING DATE: 2000-04-28			
; NUMBER OF SEQ ID NOS: 36			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 27			
; LENGTH: 5149			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-845-416-27			
Query Match 100.0%; Score 1501; DB 10; Length 5149;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ACAATGGCAAGACCTCCAAAGGTGAAATTGAAGTTCACACAGATGTTTATCAACAACCTGGA	60
Db	2908	ACAATGGCAAGACCTCCAAAGGTGAAATTGAAGTTCACACAGATGTTTATCAACAACCTGGA	2967
QY	61	TGAAAACAGCCAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTATCA	120
Db	2968	TGAAAACAGCCAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTATCA	3027
QY	121	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT	180
Db	3028	AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAGAAAGTCTCTCAACAT	3087
QY	181	TAGGTCCCATTTGGAAGCCAGTTCTTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA	240
Db	3088	TAGGTCCCATTTGGAAGCCAGTTCTTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA	3147
QY	241	ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG	300
Db	3148	ACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG	3207
QY	301	CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA	360
Db	3208	CGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA	3267
QY	361	AACTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA	420
Db	3268	AACTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA	3327
QY	421	GCCTTTGGAAGGACTAGAGAAAATCTTACCAGGAGCCACAGAGAGTGCCTCCTGAGGAGAG	480
Db	3328	GCCTTTGGAAGGACTAGAGAAAATCTTACCAGGAGCCACAGAGAGTGCCTCCTGAGGAGAG	3387
QY	481	AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGTTGAGGAGGTCAATACTGAGTGGGA	540
Db	3388	AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGTTGAGGAGGTCAATACTGAGTGGGA	3447
QY	541	AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT	600
Db	3448	AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACT	3507
QY	601	CCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT	660

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Db 3508 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 3567
QY 661 CAAGGGATCCTGGCAGCCCGTGGCGCATCTCCTCATTGACTCTCTCCAAGATCACCTCGA 720
Db 3568 CAAGGGATCCTGGCAGCCCGTGGCGCATCTCCTCATTGACTCTCTCCAAGATCACCTCGA 3627
QY 721 GAAAGTCAAGGCACTTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTGAGCCACGTCAA 780
Db 3628 GAAAGTCAAGGCACTTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTGAGCCACGTCAA 3687
QY 781 TGACCTTGCTCGCAGCTTACCACCTTTGGGCATTGAGCTCTCACCGTATAACCTCAGCAC 840
Db 3688 TGACCTTGCTCGCAGCTTACCACCTTTGGGCATTGAGCTCTCACCGTATAACCTCAGCAC 3747
QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCGTGCAGGACCGAGTCAG 900
Db 3748 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCGTGCAGGACCGAGTCAG 3807
QY 901 GCAGCTGCATGAAGCCCAACAGGCACTTTGGTCCAGCATCTCAGCACCTTCTTTCCACGTC 960
Db 3808 GCAGCTGCATGAAGCCCAACAGGCACTTTGGTCCAGCATCTCAGCACCTTCTTTCCACGTC 3867
QY 961 TGTCCAGGTCCTTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020
Db 3868 TGTCCAGGTCCTTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 3927
QY 1021 CGAGACTCAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db 3928 CGAGACTCAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 3987
QY 1081 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 3988 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 4047
QY 1141 GAAGGCCCTTGTCTGGATCTCTGAGCCCTGTGAGCTGATGATGCTTGGACCAAGCA 1200
Db 4048 GAAGGCCCTTGTCTGGATCTCTGAGCCCTGTGAGCTGATGATGCTTGGACCAAGCA 4107
QY 1201 CAACCTCAAGCAAAATGACCCCATGGATATCCTGCAGATTATTAATTGTTGACCAAC 1260
Db 4108 CAACCTCAAGCAAAATGACCCCATGGATATCCTGCAGATTATTAATTGTTGACCAAC 4167
QY 1261 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGGGTGGA 1320
Db 4168 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGGGTGGA 4227
QY 1321 TATGTGCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1380
Db 4228 TATGTGCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 4287
QY 1381 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGACACATTTGGAAGACAAAGTACAG 1440
Db 4288 CCTGTCTTTAAACTGGCATCATTTCCCTGTGTAAAGACACATTTGGAAGACAAAGTACAG 4347
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGGCCT 1500
Db 4348 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGGCCT 4407
QY 1501 C 1501
Db 4408 C 4408
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RESULT 13

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US-10-149-736-40
; Sequence 40, Application US/10149736
; Publication No. US20030216332A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Harper, Scott Q.
; TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
; FILE REFERENCE: UM-06968
; CURRENT APPLICATION NUMBER: US/10/149,736
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; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/31126
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,848
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 5339
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-149-736-40
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Query Match 100.0%; Score 1501; DB 16; Length 5339;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATGGCAAGACCTCCAAGGTGAAATTTGAAGCTCACACAGATGTTTATCACAACTGGA 60
Db 1693 ACAATGGCAAGACCTCCAAGGTGAAATTTGAAGCTCACACAGATGTTTATCACAACTGGA 1752
QY 61 TGAACACAGCCAAATAATCCTGAGATCCCTGGAAGTTCCGATGATGAGTCTCTGTACA 120
Db 1753 TGAACACAGCCAAATAATCCTGAGATCCCTGGAAGTTCCGATGATGAGTCTCTGTACA 1812
QY 121 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTTCGAAAAAGTCTCTCAACAT 180
Db 1813 AAGACGTTTGGATAACATGAACCTCAAGTGGAGTGAACCTTCGAAAAAGTCTCTCAACAT 1872
QY 181 TAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 1873 TAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGA 1932
QY 241 ACTTCTGGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db 1933 ACTTCTGGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 1992
QY 301 CGACTTTCCAGCAGTTTCAGAACGACGATGTACATAGGCGCTTCAAGAGGGAATTGAA 360
Db 1993 CGACTTTCCAGCAGTTTCAGAACGACGATGTACATAGGCGCTTCAAGAGGGAATTGAA 2052
QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db 2053 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 2112
QY 421 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 480
Db 2113 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCAGAGAGCTGCCTCCTGAGGAGAG 2172
QY 481 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 540
Db 2173 AGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 2232
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 600
Db 2233 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACT 2292
QY 601 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGAT 660
Db 2293 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGAT 2352
QY 661 CAAGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
Db 2353 CAAGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 2412
QY 721 GAAACTCAAGGCACCTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGTGAGCCACGTCAA 780
Db 2413 GAAACTCAAGGCACCTTCGAGGAGAAATTTGGCCCTCTGAAAGAGAACGTGAGCCACGTCAA 2472
QY 781 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCATTGAGCTCTCACCGTATAACCTCAGCAC 840
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Db 2473 TGACCTTTGCTCGCCAGCTTACCACCTTTGGGCATTGAGCTCTCACCGTATAACCTCAGCAC 2532
QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTTCTGCAGGTGGCCGTGAGGACCGAGTCAG 900
Db 2533 TCTGGAAGACCTGAACACACAGATGGAAGCTTTCTGCAGGTGGCCGTGAGGACCGAGTCAG 2592
QY 901 GCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 960
Db 2593 GCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTC 2652
QY 961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA 1020
Db 2653 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCA 2712
QY 1021 CGAGACTCAAAACAATGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGC 1080
Db 2713 CGAGACTCAAAACAATGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGC 2772
QY 1081 TGACCTGAATAATGTCAGATTCTCAGCTTATAGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 2773 TGACCTGAATAATGTCAGATTCTCAGCTTATAGACTGCCATGAAACTCCGAAGACTGCA 2832
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGACGCTGCATGTGATGCCCTTGACACGCA 1200
Db 2833 GAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGACGCTGCATGTGATGCCCTTGACACGCA 2892
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATGTTTGACCCAC 1260
Db 2893 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATGTTTGACCCAC 2952
QY 1261 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 1320
Db 2953 TATTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGA 3012
QY 1321 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1380
Db 3013 TATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 3072
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Db 3073 CCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 3132
QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGAGCGGCTGGGCCT 1500
Db 3133 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGAGCGGCTGGGCCT 3192
QY 1501 C 1501
Db 3193 C 3193

RESULT 14
US-10-149-736-41
; Sequence 41, Application US/10149736
; Publication No. US20030216332A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Harper, Scott Q.
; TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
; FILE REFERENCE: UM-06968
; CURRENT APPLICATION NUMBER: US/10/149,736
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/31126
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,848
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 5462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic
US-10-149-736-41
Query Match 100.0%; Score 1501; DB 16; Length 5462;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTTATCAACACCTTGA 60
Db 1816 ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTTATCAACACCTTGA 1875
QY 61 TGAAAAACAGCCAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCTCTGTTACA 120
Db 1876 TGAAAAACAGCCAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCAGTCTCTGTTACA 1935
QY 121 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAATAAGTCTCTCAACAT 180
Db 1936 AAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAATAAGTCTCTCAACAT 1995
QY 181 TAGGTCCCATTTGGAAGCCAGTTCTTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 1996 TAGGTCCCATTTGGAAGCCAGTTCTTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 2055
QY 241 ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG 300
Db 2056 ACTTCTGGTGTGGCTACAGCTGAAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGG 2115
QY 301 CGACTTTCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 360
Db 2116 CGACTTTCAGCAGTTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAA 2175
QY 361 AACTAAAGAACCTGTATATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db 2176 AACTAAAGAACCTGTATATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 2235
QY 421 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCACAGAGAGTGCCTCCTGAGGAGAG 480
Db 2236 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCACAGAGAGTGCCTCCTGAGGAGAG 2295
QY 481 AGCCCAAGATGTCACTCGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 540
Db 2296 AGCCCAAGATGTCACTCGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGA 2355
QY 541 AAAATTGAACCTGCACCTCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACT 600
Db 2356 AAAATTGAACCTGCACCTCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACT 2415
QY 601 CCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 660
Db 2416 CCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGAT 2475
QY 661 CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 720
Db 2476 CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGA 2535
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAAATTGCGCCTCTGAAAAGAGAACGTGAGCCACGTCAA 780
Db 2536 GAAAGTCAAGGCACCTTCGAGGAGAAAATTGCGCCTCTGAAAAGAGAACGTGAGCCACGTCAA 2595
QY 781 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 840
Db 2596 TGACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCAC 2655
QY 841 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAG 900
Db 2656 TCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAG 2715
QY 901 GCAGCTGCATGAAGCCCAAGGGACTTTGGTCCAGATCTCAGCACTTTCTTTCCACGTC 960
Db 2716 GCAGCTGCATGAAGCCCAAGGGACTTTGGTCCAGATCTCAGCACTTTCTTTCCACGTC 2775
QY 961 TGTCCAGGTCCCTGGGAGAGAGCCCATCTCGCCAAAACAAAGTCCCCTACTATATCAACCA 1020

Db 2776 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 2835
QY 1021 CGAGACTCAACAACTTGTCTGGGACCATCCCAAAATGACAGAGTCTACCAGTCTTTAGC 1080
Db 2836 CGAGACTCAACAACTTGTCTGGGACCATCCCAAAATGACAGAGTCTACCAGTCTTTAGC 2895
QY 1081 TGACCTGAATATGTCTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 1140
Db 2896 TGACCTGAATATGTCTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 2955
QY 1141 GAAGGCCCTTTGGCTTGGATCTCTTGAGCCTGTCTCAGCTGCTGATGCTTGGACCAAGCA 1200
Db 2956 GAAGGCCCTTTGGCTTGGATCTCTTGAGCCTGTCTCAGCTGCTGATGCTTGGACCAAGCA 3015
QY 1201 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAAC 1260
Db 3016 CAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAAC 3075
QY 1261 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAAGTCCCTCTCTGCGGTGGA 1320
Db 3076 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAAGTCCCTCTCTGCGGTGGA 3135
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QY 1441 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGCTGGCCCT 1500
Db 3256 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGCTGGCCCT 3315
QY 1501 C 1501
Db 3316 C 3316

RESULT 15
US-10-149-736-42
; Sequence 42, Application US/10149736
; Publication No. US20030216332A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Harper, Scott Q.
; TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
; FILE REFERENCE: UM-06968
; CURRENT APPLICATION NUMBER: US/10/149,736
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/31126
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,848
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 8689
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-149-736-42

Query Match 100.0%; Score 1501; DB 16; Length 8689;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAATGGCAAGACCTCCAAAGTGAATTTGAAGCTCACACAGATGTTTATCAACACCTGGA 60
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Db 3208 TGAAACACAGCCAAACAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCTCTGTACA 3267
QY 121 AAGACGTTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAGAGTCTCTCAACAT 180
Db 3268 AAGACGTTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAAGAGTCTCTCAACAT 3327
QY 181 TAGGTCCCATTTGGAAAGCCAGTTCTGACCAAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 240
Db 3328 TAGGTCCCATTTGGAAAGCCAGTTCTGACCAAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGA 3387
QY 241 ACTTCTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 300
Db 3388 ACTTCTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGG 3447
QY 301 CGACTTTCCAGCAGTTTCAGAAAGCAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 360
Db 3448 CGACTTTCCAGCAGTTTCAGAAAGCAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 3507
QY 361 AACTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA 420
Db 3508 AACTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCA 3567
QY 421 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCCAGAGAGTGCCTCCTGAGGAGAG 480
Db 3568 GCCTTTGGAAGGACTAGAGAACTCTACAGGAGCCCAGAGAGTGCCTCCTGAGGAGAG 3627
QY 481 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGAGGTTCAATACTGAGTGGGA 540
Db 3628 AGCCCAAGATGTCACTCGGCTTCTACGAAAGCAGGCTGAGAGGTTCAATACTGAGTGGGA 3687
QY 541 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAATAGATGAGACCTTTGAAAGACT 600
Db 3688 AAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAATAGATGAGACCTTTGAAAGACT 3747
QY 601 CCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 660
Db 3748 CCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 3807
QY 661 CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCAGCTCGA 720
Db 3808 CAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCAGCTCGA 3867
QY 721 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCCTCTGAAAGAGAACGTTGAGGCCACGTCAA 780
Db 3868 GAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCCTCTGAAAGAGAACGTTGAGGCCACGTCAA 3927
QY 781 TGACCTTGCTCGCCAGCTTACACATTTTGGGCATTTGAGCTTACCGTATACCTCAGCAC 840
Db 3928 TGACCTTGCTCGCCAGCTTACACATTTTGGGCATTTGAGCTTACCGTATACCTCAGCAC 3987
QY 841 TCTGGAAGACCTGAAACACCAAGTGAAGCTTCTGAGTGGCCGTCGAGGACCGAGTCAG 900
Db 3988 TCTGGAAGACCTGAAACACCAAGTGAAGCTTCTGAGTGGCCGTCGAGGACCGAGTCAG 4047
QY 901 GCAGCTGCATGAAGCCCAACAGGACTTTTGGTCCAGCATCTCTCAGCACCTTTCTTCCACGTC 960
Db 4048 GCAGCTGCATGAAGCCCAACAGGACTTTTGGTCCAGCATCTCTCAGCACCTTTCTTCCACGTC 4107
QY 961 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 1020
Db 4108 TGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCA 4167
QY 1021 CGAGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1080
Db 4168 CGAGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 4227
QY 1081 TGACCTGAATAATGTCTCAGATTCTCAGCTTATAGGACTGCGATGAAACTCCGAGAGACTGCA 1140
Db 4228 TGACCTGAATAATGTCTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAGAGACTGCA 4287
QY 1141 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGTGCATGTGATGCCTTGGACCAAGCA 1200

Db	4288	GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCA	4347
QY	1201	CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCCAC	1260
Db	4348	CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCCAC	4407
QY	1261	TATTTATAGCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGA	1320
Db	4408	TATTTATAGCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGA	4467
QY	1321	TATGTGCTGAAGCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT	1380
Db	4468	TATGTGCTGAAGCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT	4527
QY	1381	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	1440
Db	4528	CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG	4587
QY	1441	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCT	1500
Db	4588	ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCT	4647
QY	1501	C	1501
Db	4648	C	4648

Search completed: September 19, 2004, 15:14:15
Job time : 504.133 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 02:48:31 ; Search time 2714.88 Seconds
(without alignments)
16510.166 Million cell updates/sec

Title: US-09-845-416-10_COPY_1500_3000
Perfect score: 1501
Sequence: 1 acaatggcagacctccaag.....accagcgaggctgggcctc 1501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				EST:*			
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				2:	em_esthum:*		
				3:	em_estin:*		
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				5:	em_estov:*		
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				16:	em_estom:*		
				17:	em_gss_hum:*		
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				27:	em_gss_vrl:*		
				28:	gb_gss1:*		
				29:	gb_gss2:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515.6	34.4	3753	11 AK081426	AK081426 Mus muscu
2	491.2	32.7	2874	29 AY408546	AY408546 Homo sapi
3	486.6	32.4	579	9 AL121550	AL121550 DKFZp762L
4	484	32.2	777	14 CD653550	CD653550 AGENCOURT

5	484	32.2	824	9	AL556247
6	482.4	32.1	801	14	CB991394
7	482.4	32.1	1098	13	BX365572
8	482	32.1	797	14	CB960722
9	477.6	31.8	2874	29	AY408548
10	475	31.6	834	12	BI729851
11	473	31.5	620	13	BQ640063
12	462.8	30.8	508	14	CD701871
13	455.8	30.4	591	13	BX490860
14	450.4	30.0	770	12	BG719710
15	439	29.2	578	13	BX485574
16	435	29.0	652	10	BB629984
17	435	29.0	1298	11	AK087829
18	435	29.0	2135	11	AK013510
19	435	29.0	4437	11	AK036936
20	433.4	28.9	1384	11	AK075809
21	430.2	28.7	704	10	BB610411
22	420.4	28.0	750	12	BI730168
23	420.2	28.0	512	14	CF162938
24	417.4	27.8	663	12	BM488464
25	412.4	27.5	854	9	AI196693
26	410.4	27.3	599	10	BB666688
27	410.2	27.3	3051	11	BC036095
28	407.2	27.1	554	14	CB613696
29	406.6	27.1	665	13	BY742604
30	406.2	27.1	520	29	CG606443
31	404.4	26.9	493	14	CA888041
32	397.4	26.5	495	14	CA894775
33	389	25.9	644	13	BU313510
34	385.6	25.7	650	13	BY714491
35	383.4	25.5	483	14	CA893902
36	381.8	25.4	423	9	AA460476
37	381.8	25.4	513	29	CG605968
38	380.8	25.4	508	29	CG606947
39	379.4	25.3	717	14	CB527785
40	369.8	24.6	488	29	CG597965
41	369.8	24.6	542	29	CG594848
42	369.2	24.6	502	9	AL871560
43	367.8	24.5	677	9	AL641565
44	366.2	24.4	622	9	AL796733
45	365.2	24.3	2874	29	AY408547

ALIGNMENTS

RESULT 1	AK081426	AK081426	3753 bp	mrna	linear	HTC 20-SEP-2003
LOCUS	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30016K19 product:dystrophin related protein 2, full insert sequence.					
DEFINITION	AK081426					
ACCESSION	AK081426					
VERSION	AK081426.1 GI:26349154					
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1					
AUTHORS	Carninci,P. and Hayashizaki,Y.					
TITLE	High-efficiency full-length cDNA cloning					
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)					
MEDLINE	99279253					
PUBMED	10349636					
REFERENCE	2					
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.					
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes					
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)					
MEDLINE	20499374					
PUBMED	11042159					

AL556247	AL556247
CB991394	AGENCOURT
BX365572	BX365572
CB960722	AGENCOURT
AY408548	Mus muscu
BI729851	603349511
BQ640063	he23g04.Y
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BX485574	DKFZp686L
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AK013510	Mus muscu
AK036936	Mus muscu
AK075809	Mus muscu
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BI730168	603349711
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BM488464	pgm2n.pk0
AI196693	ui53e10.Y
BB666688	BB666688
BC036095	Homo sapi
CB613696	AMGNNUC:N
BY742604	BY742604
CG606443	OST284316
CA888041	B0142C06-
CA894775	B0187G06-
BU313510	603540290
BY714491	BY714491
CA893902	B0182B01-
AA460476	zx61e10.Y
CG605968	OST283399
CG606947	OST285335
CB527785	UI-M-FY0-
CG597965	OST261937
CG594848	OST253426
AL871560	AL871560
AL641565	AL641565
AL796733	AL796733
AY408547	Pan trogl

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c lone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: NDAM513 row: a column: 23
High quality sequence stop: 715.

FEATURES

source

Location/Qualifiers
1. 777
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30426742"
/tissue type="Embryonic Stem cells"
/cell_line="WA01"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library (Long)"
/note="Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI;
This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01 cell line . Undifferentiated human ES cell line WA01/H1 was obtained from Wicell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIzol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199] Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGCGCGCCCTTTT-3'] from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex tag polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

ORIGIN

Query Match 32.2%; Score 484; DB 14; Length 777;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1018 CCACGAGACTCAAACAACCTGCTGGGACCATCCCAAATGACAGAGCTCTACCGTCTTT 1077
Db 137 CCACGAGACTCAAACAACCTGCTGGGACCATCCCAAATGACAGAGCTCTACCGTCTTT 196
Qy 1078 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 1137
Db 197 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 256
Qy 1138 GCAGAAGGCCCTTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCTTGGACCA 1197
Db 257 GCAGAAGGCCCTTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCTTGGACCA 316
Qy 1198 GCACAACCTCAAGCAAAATGACCAAGCCCATGGATATCCTGACAGATTATTATTGTTTGAC 1257
Db 317 GCACAACCTCAAGCAAAATGACCAAGCCCATGGATATCCTGACAGATTATTATTGTTTGAC 376
Qy 1258 CACTATTTATGACCGCCTGGAGCAAGAGCACAAACATTTGGTCAACGTCCTCTCTGCGT 1317
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Db 437 GGATATGTGTCGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCG 496
Qy 1378 TGTCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAGTA 1437
Db 497 TGTCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAGTA 556
Qy 1438 CAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAGCGCAGGCTGG 1497
Db 557 CAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAGCGCAGGCTGG 616
Qy 1498 CCTC 1501
Db 617 CCTC 620

RESULT 5

AL556247

LOCUS

DEFINITION

AL556247 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens

AL556247

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL556247 824 bp mRNA linear EST 31-MAY-2003
AL556247 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CSODK001YB17 5-PRIME, mRNA sequence.

AL556247
AL556247.2 GI:31278051
EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 824)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12898746.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1955.r

Contact.: Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODK001CA09QF1.

Location/Qualifiers

1. 824

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODK001YB17"

/cell_type="HELA CELLS COT 25-NORMALIZED"

/cell_line="HELA"

/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 32.2%; Score 484; DB 9; Length 824;
Best Local Similarity 100.0%; Pred. No. 2.1e-132;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1018 CCACGAGACTCAAACAACCTGCTGGGACCATCCCAAATGACAGAGCTCTACCGTCTTT 1077
Db 195 CCACGAGACTCAAACAACCTGCTGGGACCATCCCAAATGACAGAGCTCTACCGTCTTT 254
Qy 1078 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 1137
Db 255 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 314
Qy 1138 GCAGAAGGCCCTTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCTTGGACCA 1197

Db 315 GCAGAAGGCCCTTTCTGTTGGATCTCTTGAGCCTGTGCAGCTGCATGTGATGCCTTGGACCA 374

QY 1198 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1257

Db 375 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 434

QY 1258 CACTATTATGACCGCCTGGAGCAAGAGACAACAATTTGGTCAACGTCCTCTCTGCGT 1317

Db 435 CACTATTATGACCGCCTGGAGCAAGAGACAACAATTTGGTCAACGTCCTCTCTGCGT 494

QY 1318 GGATATGTGTGAAGTGGCTGCTGATGTTTATGATACGGGACGAGGAGGATCCG 1377

Db 495 GGATATGTGTGAAGTGGCTGCTGATGTTTATGATACGGGACGAGGAGGATCCG 554

QY 1378 TGTCTGTCTTTAAACTGGCATCTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1437

Db 555 TGTCTGTCTTTAAACTGGCATCTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 614

QY 1438 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGG 1497

Db 615 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGG 674

QY 1498 CCTC 1501

Db 675 CCTC 678

RESULT 6

CB991394

LOCUS

DEFINITION

AGENCOURT_13627932 NIH_MGC_148 Homo sapiens CDNA clone

IMAGE:30336570 5', mRNA sequence.

CB991394

CB991394.1 GI:30285818

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 801)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: NDA360 row: d column: 19

High quality sequence stop: 621.

Location/Qualifiers

1. .801

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30336570"

/tissue_type="pre-eclampsic placenta"

/lab_host="DH10B Tona"

/clone_lib="NIH_MGC_148"

/note="Organ: Placenta; Vector: pBluescriptR; Site_1: all-XhoI; Site_2: BamHI; Library is oligo-dt primed and directionally cloned using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC

Library."

ORIGIN

Query Match 32.1%; Score 482.4; DB 14; Length 801;

Best Local Similarity 99.8%; Pred. No. 6.1e-132;

Matches 483; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1018 CCACGAGACTCAAACTTGTCTGGGACCATCCAAAATGACAGAGCTCTACCACTCTT 1077

Db 140 CCACGAGACTCAAACTTGTCTGGGACCATCCAAAATGACAGAGCTCTACCACTCTT 199

QY 1078 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 1137

Db 200 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 259

QY 1138 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGATGATGCTTGGACCA 1197

Db 260 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGATGATGCTTGGACCA 319

QY 1198 GCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTGAC 1257

Db 320 GCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAATTGTTGAC 379

QY 1258 CACTATTATGACCGCCTTGGAGCAAGAGACAACTTTGTTCAACGTCCTCTCTGCGT 1317

Db 380 CACTATTATGACCGCCTTGGAGCAAGAGACAACTTTGTTCAACGTCCTCTCTGCGT 439

QY 1318 GGATATGTGTGAAGTGGCTGCTGTAATGTTTATGATACGGGACGAGGAGGATCCG 1377

Db 440 GGATATGTGTGAAGTGGCTGCTGTAATGTTTATGATACGGGACGAGGAGGATCCG 499

QY 1378 TGTCTGTCTTTAAACTGGCATCTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1437

Db 500 TGTCTGTCTTTAAACTGGCATCTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 559

QY 1438 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGG 1497

Db 560 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGG 619

QY 1498 CCTC 1501

Db 620 CCTC 623

RESULT 7

CB991394

LOCUS

DEFINITION

AGENCOURT_13627932 NIH_MGC_148 Homo sapiens CDNA clone

IMAGE:30336570 5', mRNA sequence.

CB991394

CB991394.1 GI:30366927

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1098)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to cluster 1955.r

Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/InvitrogenCorporation1600>

Faraday Avenue Genoscope sequence ID: CSI:AK001ZB11QPI.

Location/Qualifiers

1. .1098

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="CS0DK001YB21"
/cell_type="HELA CELLS COT 25-NORMALIZED"
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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 32.1%; Score 482.4; DB 13; Length 1098;
Best Local Similarity 99.8%; Pred. No. 7.7e-132;
Matches 483; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1018 CCACGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTT 1077
Db |||||
204 CCACGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTT 263
QY 1078 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 1137
Db |||||
264 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 323
QY 1138 GCAGAAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGTCATGTGATGCCCTTGGACCA 1197
Db |||||
324 GCAGAAAGGCCCTTTGCTTGGKTCCTTGAGCCCTGTGAGCTGTCATGTGATGCCCTTGGACCA 383

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Db |||||
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QY 1258 CACTATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGT 1317
Db |||||
444 CACTATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGT 503

QY 1318 GGATATGTGCTGAATGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCG 1377
Db |||||
504 GGATATGTGCTGAATGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCG 563

QY 1378 TGTCCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1437
Db |||||
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QY 1438 CAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGCTGGG 1497
Db |||||
624 CAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGCTGGG 683

QY 1498 CCTC 1501
Db |||||
684 CCTC 687

RESULT 8

CB960722
LOCUS CB960722
DEFINITION AGENCOURT_13761995 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30344479 5', mRNA sequence.
ACCESSION CB960722
VERSION CB960722.1 GI:30216839
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

797 bp mRNA linear EST 29-APR-2003

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 797)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM380 row: n column: 08
High quality sequence stop: 620.

Location/Qualifiers

FEATURES

source

1..797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30344479"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
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5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Query Match 32.1%; Score 482; DB 14; Length 797;
Best Local Similarity 100.0%; Pred. No. 8.1e-132;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 CCACGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTT 1077
Db |||||
168 CCACGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTT 227

QY 1078 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 1137
Db |||||
228 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 287

QY 1138 GCAGAAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGTCATGTGATGCCCTTGGACCA 1197
Db |||||
288 GCAGAAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGTCATGTGATGCCCTTGGACCA 347

QY 1198 GCACAACTCAAGCAAAATGACCAAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1257
Db |||||
348 GCACAACTCAAGCAAAATGACCAAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 407

QY 1258 CACTATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGT 1317
Db |||||
408 CACTATTTATGACCGCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGT 467

QY 1318 GGATATGTGCTGAATGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCG 1377
Db |||||
468 GGATATGTGCTGAATGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCG 527

QY 1378 TGTCCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1437
Db |||||
528 TGTCCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 587

QY 1438 CAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGCTGGG 1497
Db |||||
588 CAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGCTGGG 647

QY 1498 CC 1499

Db |||

648 CC 649

RESULT 9

AY408548

LOCUS

DEFINITION

AY408548 2874 bp DNA linear GSS 15-DEC-2003
Mus musculus DRP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY408548
VERSION AY408548.1 GI:39764519
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2874)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2874)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source Location/Qualifiers
1..2874
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1..>2874
/gene="DRP2"
ORIGIN
/locus_tag="HCM3260"
Query Match 31.8%; Score 477.6; DB 29; Length 2874;
Best Local Similarity 57.7%; Pred. No. 4.2e-130;
Matches 786; Conservative 0; Mismatches 576; Indels 0; Gaps 0;
QY 136 CATGAACCTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGA 195
DB 234 CATGAATCTGTGTGAATGAATAAAAAAGAAAGTCTCAACAACCTCCGGCTCGCCTAGA 293
QY 196 AGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGACGAACTTCTGGTGTGGCT 255
DB 294 GGCCTTCTCAGACCTCAGTGGAAAACTTCAGCTCCCGCTCCGAGAGATTATTGACTGGCT 353
QY 256 ACAGCTGAAGATGATGAATTAAGCCGCGCAGGCACCTATTGGAGGCGACTTTCCAGCAGT 315
DB 354 CAGCCAAAAGGATGAGGAGTTGTCAAGCTCAGCTCCCTTGAAGGGGATGTGGCCCTGGT 413
QY 316 TCAGAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAAAACTAAAGAACCTGT 375
DB 414 ACAACAGGAGAAGGAGACACATGACGCTTCATGGAAGAGTCAAGTCTAAGGGCCCTA 473
QY 376 AATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTTGGAGGACT 435
DB 474 CATCTCCTCTGTGCTTGAATCCGCCCCAGGCTTTTCTGTCCAGCATCCATTTTGAAGAATT 533
QY 436 AGAGAACTCTACAGGAGCCCGCAGAGAGTGCCTCTGAGGAGAGAGCCCGAGATGTCAAC 495
DB 534 AGAGGAGTCTCAATCTGAGAGTAAAGATACCTCCCGCAGACAGCGGATTCAAAAACCTTAG 593
QY 496 TCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACCTAGTGGGAAAAATTGAACCTGCA 555
DB 594 TCGCTTTGTATGGAAGCAGGCAACAGTGGCCAGTGTGAGCTGTGGGAGAGCTGACAGCCCG 653
QY 556 CTCGCGTCACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGAGACTCCAGGAACCTCAAGA 615
DB 654 CTGTGTAGATCAGCATCGCCCAATTGAGCATACTCTGGAACATCTATTGGAGATCCAAGG 713
QY 616 GGCCACGGATGAGCTGGACCTCAAGCTCGGCCAAGCTGAGGTGATCAAGGGATCCTGGCA 675

DB 714 GGCAATGGAGGAATTGAGCAGTACTTTTGACCAAGCAGAGGGAGTCCGAGCCACGTGGGA 773
QY 676 GCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGAAAGTCAAGGCACT 735
DB 774 GCCCATAGGAGATCTCTTTATTGATTCCTCCAGAGCATATCCAAAGCCATCAAGCTATT 833
QY 736 TCGAGGAGAAATTGGCCCTCTGAAAGAGAAAGTGAAGCCAGTCAATGACCTTGTCTCGCCA 795
DB 834 CAAGAAGAATTCTCTCTCTGTAAGATGGGGTGAAGTTAGTGAATGATCTGGCCCCACCA 893
QY 796 GCTTACCACCTTTGGGCATTTCAGCTCTCACCCTGATAACCTCAGCACTCTGGAAGACCTGAA 855
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QY 856 CACCAGATGGAAGCTTCTGAGGTGGCCCTCGAGGACCGAGTCAGGAGCTGCATGAAGC 915
DB 954 CATCCGTTGGAACAGCTCCAGGTGTCACTGGCTGAGAGGCTTAAGCAACTCCAGGATGC 1013
QY 916 CCACAGGACCTTTGGTCCAGCATCTCAGCACTTTCTTCCACGCTGTCTCCAGGGTCCCTG 975
DB 1014 CCACCGGACCTTTGGCCCTGGGTCAAGCACTTCTCTCCACTTCTGTCCAAGTTCCCTG 1073
QY 976 GGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCAGGAGACTCAAAACAAC 1035
DB 1074 GGAAGAGACAAATTTCTCCCAATAAAGTCCCTACTACATCAANNNNNNNNNNNNNN 1133
QY 1036 TTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGT 1095
DB 1134 NNN 1193
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DB 1194 TAAGTTCTCAGCTTACCGCACTGCCATGAAGCTCCGAGAGTCCAGAAAGGCCCTTGGCCT 1253
QY 1156 GGATCTCTGAGCCTGTGAGCTGCATGTGATGCTTGGACCAAGCAACCTCAAGCAAAA 1215
DB 1254 GGATCTGGTAACTTTAACTACAGCTCTGGAGATCTTCAATGAGCATGACTTGCAGGCCAG 1313
QY 1216 TGACCAAGCCCATGGATATCCTGCAGATTATTAAATTTGTTGACCACTATTATGACCGCT 1275
DB 1314 TGAACATGTGATGATGTGGTGGAGTCACTTCACTGCTGACTGCTTGTATGAACGACT 1373
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QY 1336 GCTGCTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGTGCTCTTTTAAAC 1395
DB 1434 GCTCCTCAATGTTTTTGTATAGTGTGCGAGTGGAAAGATGCGAGCATTTGCTTTAAGAC 1493
QY 1396 TGGCATCATTTCCCTGTGTAAGCACATTTTGAAGACAGTACAGATACCTTTTCAAGCA 1455
DB 1494 TGGCATCGCATGCCTGTGTGGCAGGAAAGTGAAGAAAAAACTTCAGTATCTCTTCAGCCA 1553
QY 1456 AGTGGCAAGTTCAACAGGATTTTGTGACCGAGCGGCTGGG 1497
DB 1554 AGTAGCCAAATTCAGGCAGCCAGTGTGATCAACGCCATCTCGG 1595
RESULT 10
BI729851
LOCUS 603349511P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5357162 5',
DEFINITION mRNA sequence.
ACCESSION BI729851
VERSION BI729851.1 GI:15706864
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 834)

Db 121 TTGCTTGGATCTCTTGAGCCTGTGACGCTGCATGTGATGCCTTGGACGACACAACCTCA 180
QY 1209 AGCAAAATGACCAAGCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTATG 1268
Db 181 AGCAAAATGACCAAGCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTATG 240
QY 1269 ACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGC 1328
Db 241 ACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGC 300
QY 1329 TGAACCTGGCTGCTGAATGTTTATGATACGGGACCAACAGGGAGGATCCGTGTCTGCTT 1388
Db 301 TGAACCTGGCTGCTGAATGTTTATGATACGGGACCAACAGGGAGGATCCGTGTCTGCTT 360
QY 1389 TTAACACTGGCATCTATTTCCCTGTGTAAAGCACATTTGGAAGACAACTACAGATACCTTT 1448
Db 361 TTAACACTGGCATCTATTTCCCTGTGTAAAGCACATTTGGAAGACAACTACAGATACCTTT 420
QY 1449 TCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTC 1501
Db 421 TCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTC 473

RESULT 12
CD701871
LOCUS CD701871 508 bp mRNA linear EST 25-JUN-2003
DEFINITION EST18395 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD701871
VERSION CD701871.1 GI:32232501
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 508)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1. 508
/organism="Homo sapiens"
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library from southern Chinese"

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ORIGIN
Query Match 30.8%; Score 462.8; DB 14; Length 508;
Best Local Similarity 99.6%; Pred. No. 3.1e-126;
Matches 464; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1036 TTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAAGTCTTAGCTGACCTGAATAATGT 1095
Db 16 TTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAAGTCTTAGCTGACCTGAATAATGT 75
QY 1096 CAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTT 1155
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QY 1156 GGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCACAACTCAAGCAAAA 1215
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QY 1216 TGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTATGACCGCCT 1275
Db 196 TGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTATGACCGCCT 255
QY 1276 GGAGCAAGAGCACACAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGTGAACCTG 1335
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QY 1336 GCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGTCTGCTTTTAAAC 1395
Db 316 GCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGTCTGCTTTAATAAC 375
QY 1396 TGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCA 1455
Db 376 TGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCA 435
QY 1456 AGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTC 1501
Db 436 AGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTC 481

RESULT 13
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LOCUS BX490860 591 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFP686F1392 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION DKFP686F1392.5, mRNA sequence.
VERSION BX490860
KEYWORDS BX490860.1 GI:32000785
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 591)
Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Dueseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKFP686F1392) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 591
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="DKFP686F1392"
/dev_stage="adult"
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/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

FEATURES
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1. 591
/organism="Homo sapiens"
/mol_type="mRNA"
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/dev_stage="adult"
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cDNA-collection"

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Best Local Similarity 99.3%; Pred. No. 4.3e-124;
Matches 457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1018 CCACGAGACTCAAAACACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTTT 1077
Db 132 CCACGAGACTCAAAACACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTTT 191
QY 1078 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACT 1137

Db 192 AGCTGACCTGAATAATGTAGATTTCTCAGCTTATAGGAGTCCATGAAACTCCGAAGACT 251

QY 1138 GCAGAAAGCCCTTTGCTTGGATCTCTTGGCCCTGTGAGCCTGTGAGCTGCATGTGATGCCCTTGGACCA 1197

Db 252 GCAGAAAGCCCTTTGCTTGGATCTCTTGGCCCTGTGAGCCTGTGAGCTGCATGTGATGCCCTTGGACCA 311

QY 1198 GCACAACTCAAGCAAAATGACCAAGCCCATGGATATCCTGACAGATTATTAATTGTTGAC 1257

Db 312 GCACAACTCAAGCAAAATGACCAAGCCCATGGATATCCTGACAGATTATTAATTGTTGAC 371

QY 1258 CACTATTATGACCGCCTGGAGCAAGACGACAACTTTGTCAACGTCCTCTCTGCGT 1317

Db 372 CACTATTATGACCGCCTGGAGCAAGACGACAACTTTGTCAACGTCCTCTCTGCGT 431

QY 1318 GGATATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCG 1377

Db 432 GGATATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCG 491

QY 1378 TGTCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAACTA 1437

Db 492 TGTCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAACTA 551

QY 1438 CAGATACCTTTCAAGCAAGTGGCAAGTTCACACAGGATTT 1477

Db 552 CAGATACCTTTCAAGCANGTGGCAAGTTCACACAGGATTT 591

RESULT 14

LOCUS BG719710

DEFINITION 602690430F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4822807 5', mRNA sequence.

ACCESSION BG719710

VERSION BG719710.1 GI:13998897

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 770)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10731 row: 1 column: 08
High quality sequence stop: 767.

FEATURES

source

1..770

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4822807"

/lab_host="DH10B"

/clone_lib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescriptR (modified pBluescript Ks+); Site_1: BamHI; Site_2: SalI-XhoI (gtcag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 30.0%; Score 450.4; DB 12; Length 770;
Best Local Similarity 98.1%; Pred. No. 2.1e-122;
Matches 477; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 1018 CCACGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTT 1077

Db 150 CCACGAGACTCAAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTT 209

QY 1078 AGCTGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1137

Db 210 AGCTGACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 269

QY 1138 GCAGAAAGCCCTTTGCTTGGATCTCTTGAAGCTGTGAGCTGCATGTGATGCCCTTGGACCA 1197

Db 270 GCAGAAAGCCCTTTGCTTGGATCTCTTGAAGCTGTGAGCTGCATGTGATGCCCTTGGACCA 329

QY 1198 GCACAA--CCTCAAGCAAAATGACCAAGCCCATGGATATCCTGACAGATTATTAATTGTTT 1255

Db 330 GCACAAATCCTCAAGTCAGAATGACCAAGCCCATGGATATCCTGACAGATTATTAATTGTTT 389

QY 1256 ACCACTATTATGACCGCCTGGAGCAAGAGACAACTTTGTTGTTCAAGTCCCTCTCTGTC 1315

Db 390 ACCACTATTATGACCGCCTGGAGCAAGAGACAACTTTGTTGTTCAAGTCCCTCTCTGTC 449

QY 1316 GTGGATATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATC 1375

Db 450 GTGGATATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATC 509

QY 1376 CGTGTCTCTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAG 1435

Db 510 CGTGTCTCTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAG 569

QY 1436 TACAGATACCTTTTCAAGCAAGTGGCAAGTTCACAGGATTTTGTACCAAGCGCAGGCTG 1495

Db 570 TACAGATACCTTTTCAAGCAAGTGGCAAGTTCACAGGATTTTGTACCAAGCGCAGGCTG 628

QY 1496 GGCCTC 1501

Db 629 GGCCTC 634

RESULT 15

LOCUS BX485574

DEFINITION DKFZp686L01247_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686L01247-5', mRNA sequence.

ACCESSION BX485574

VERSION BX485574.1 GI:31948458

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 578)

AUTHORS Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.

TITLE EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)

JOURNAL Unpublished (2003)

COMMENT Contact: MIPS

MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.

This clone (DKFZp686L01247) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers

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/dev_stage="adult"
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
CDNA-collection"

ORIGIN
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Best Local Similarity 99.5%; Pred. NO. 4.3e-119;
Matches 439; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1018 CCACGAGACTCAAACTTGCTGGGACCATCCAAAATGACAGAGCTCTACCAGTCTTT 1077
Db |||||
138 CCACGAGACTCAAACTTGCTGGGACCATCCAAAATGACAGAGCTCTACCAGTCTTT 197
QY 1078 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1137
Db |||||
198 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 257
QY 1138 GCAGAAGGCCCTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCCCTTGGACCA 1197
Db |||||
258 GCAGAAGGCCCTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCCCTTGGACCA 317
QY 1198 GCACAACCTCAAGCAAAATGACCAAGCCCATGGATATCCTGACAGATTATTAATTGTTGAC 1257
Db |||||
318 GCACAACCTCAAGCAAAATGACCAAGCCCATGGATATCCTGACAGATTATTAATTGTTGAC 377
QY 1258 CACTATTATGACCGCCTGGAGCAAGCAGCACAAATTTGGTCAACGTCCCTCTCTGCGT 1317
Db |||||
378 CACTATTATGACCGCCTGGAGCAAGCAGCACAAATTTGGTCAACGTCCCTCTCTGCGT 437
QY 1318 GGATATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 1377
Db |||||
438 GGATATGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 497
QY 1378 TGTCCCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAGACAAGTA 1437
Db |||||
498 TGTCCCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATNTGGAGACAAGTA 557
QY 1438 CAGATACCTTTTCAAGCAAGT 1458
Db |||||
558 CAGATACCTTTTCAAGCAAGT 578
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Search completed: September 19, 2004, 11:02:19
Job time : 2719.88 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 18:59:56 ; Search time 3974.06 Seconds
(without alignments)
16370.617 Million cell updates/sec

Title: US-09-845-416-12_COPY_1500_3000
Perfect score: 1501
Sequence: 1 agaagatctagaacaagaac.....ttctgcatgattctatccaa 1501

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba:*
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10: gb_ro:*
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12: gb_sy:*
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41: em_htgo_other:*

Pred.No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1328.8	88.5	5339	6	AX538620	AX538620 Sequence
2	1328.8	88.5	5462	6	AX538621	AX538621 Sequence
3	1328.8	88.5	5952	6	AR304538	AR304538 Sequence
4	1328.8	88.5	5952	6	AX114289	AX114289 Sequence
5	1328.8	88.5	8689	6	AX538622	AX538622 Sequence
6	1328.8	88.5	11443	6	AX538624	AX538624 Sequence
7	1328.8	88.5	12057	6	AX538627	AX538627 Sequence
8	1328.8	88.5	12446	9	HSDMDR	X14298 Human mRNA
9	1328.8	88.5	13957	6	AX409637	AX409637 Sequence
10	1328.8	88.5	13957	6	AX538581	AX538581 Sequence
11	1328.8	88.5	13957	9	HUMDYS	M18533 Homo sapien
12	1317.8	87.8	13977	6	AR220819	AR220819 Sequence
13	1185.4	79.0	13887	4	AF070485	AF070485 Canis fam
14	1149.6	76.6	13815	6	AX306153	AX306153 Sequence
15	1149.6	76.6	13815	6	AX538582	AX538582 Sequence
16	1149.6	76.6	13815	10	MUSDYSA	M68859 Mouse dystro
17	1149.6	76.6	19307	6	AR093392	AR093392 Sequence
18	1149.6	76.6	19307	6	AR142592	AR142592 Sequence
19	1011.6	67.4	5417	6	AX538619	AX538619 Sequence
20	1006.2	67.0	4402	6	E30219	E30219 Shortened d
21	922.2	61.4	13575	5	GGDYS	X13369 Chicken mRN
22	807	53.8	4402	6	E30220	E30220 Shortened d
23	715.6	47.7	2654	5	FSCDYSTRO	M37645 Torpedo cal
24	671.4	44.7	4075	6	E30221	E30221 Shortened d
25	667.2	44.5	3747	6	E30218	E30218 Shortened d
26	613.6	40.9	3163	6	E30223	E30223 Shortened d
27	598.2	39.9	3521	5	AF339031	AF339031 Danio rer
28	555.6	37.0	10705	10	RNAJ2967	AJ002967 Rattus no
29	554.2	36.9	11096	6	AX538584	AX538584 Sequence
30	554.2	36.9	11096	10	MMY12229	Y12229 M.musculus
31	554	36.9	3161	10	MMGUTRPH	X83506 M.musculus
32	547.4	36.5	6045	6	A63605	A63605 Sequence 7
33	547.4	36.5	6045	6	AR281528	AR281528 Sequence
34	547.4	36.5	6059	6	AX107972	AX107972 Sequence
35	547.4	36.5	10302	6	AX538583	AX538583 Sequence
36	547.4	36.5	10302	9	HSMUPS	X69086 H.sapiens m
37	547.4	36.5	10320	6	A63607	A63607 Sequence 9
38	547.4	36.5	10320	6	AR281529	AR281529 Sequence
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45	505	33.6	4658	9	BC028720	BC028720 Homo sapi

ALIGNMENTS

RESULT 1
AX538620
LOCUS AX538620 5339 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 40 from Patent WO0229056.
ACCESSION AX538620
VERSION AX538620.1 GI:25271166
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
artificial sequences.
1
Chamberlain,J.S. and Harper,S.Q.
AUTHORS Mini-dystrophin nucleic acid and peptide sequences
TITLE Patent: WO 0229056-A 40 11-APR-2002;
JOURNAL THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)

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Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
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QY	222	TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG	281
Db	1935	TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG	1994
QY	282	ACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAAA	341
Db	1995	ACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAAA	2054
QY	342	CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCAGC	401
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QY	402	CTTTGGAAGGACTAGAGAAACTCTACAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAG	461
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Db	2415	AAGTCAAGGCACCTTCGAGGAGAAATTGCGCTCTGAAAGAGAACGCTGAGCCACGTCATG	2474
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Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
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QY	222	TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG	281
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LOCUS	AX538621	5462 bp	DNA linear PAT 23-NOV-2002
DEFINITION	AX538621		
ACCESSION	AX538621.1		
VERSION	GI:25271168		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	artificial sequences.		
AUTHORS	1 Chamberlain, J.S. and Harper, S.Q.		
TITLE	Mini-dystrophin nucleic acid and peptide sequences		
JOURNAL	Patent: WO 0229056-A 41 11-APR-2002;		
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Db		3195	TTCTGCATGATTCTATCCAA

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Db	2238	CTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCCAAGAGCTGCCTCCTGAGGAGAGAG	2297
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QY	822	TGGAAGACCTGAACACCAAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC	881
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RESULT 3

AR304538

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches 1333; Conservative

0; Mismatches

7; Indels

0; Gaps

0;

QY	162	GGGTTCTTTTACAAGACAGATTCTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGAAC	221
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DEFINITION Sequence 1 from Patent WO0129243.
ACCESSION AX114289
VERSION AX114289.1 GI:14031259
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Paul,X.L. and Xiao,X.
TITLE Method and vector for producing and transferring trans -spliced
peptides
JOURNAL DALHOUSIE UNIVERSITY (CA) ; UNIV. OF PITTSBURGH OF THE COMMONWEALTH
SYSTEM OF HIGHER EDUCATION (US)
PATENT: WO 0129243-A 1 26-APR-2001;
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Best Local Similarity 99.5%; Pred. No. 0;
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RESULT 5

AX538622

LOCUS

AX538622

DEFINITION

Sequence 42 from Patent WO0229056.

ACCESSION

AX538622

VERSION

AX538622.1 GI:25271171

KEYWORDS

synthetic construct

SOURCE

synthetic construct

ORGANISM

artificial sequences.

REFERENCE

1

AUTHORS

Chamberlain, J.S. and Harper, S.Q.

TITLE

Mini-dystrophin nucleic acid and peptide sequences

JOURNAL

Patent: WO 0229056-A 42 11-APR-2002;

THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)

FEATURES

Location/Qualifiers

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Query Match 88.5%; Score 1328.8; DB 6; Length 8689;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 282 ACTTTCCAGCAGTTTCAGAGCAGAACGATGTACATAGGCCCTTCAAGAGGGAATTGAAAA 341

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RESULT 6
AX538624

LOCUS AX538624 11443 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 44 from Patent WO0229056.
ACCESSION AX538624
VERSION AX538624.1 GI:25271175

SOURCE
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Chamberlain, J.S. and Harper, S.Q.
TITLE Mini-dystrophin nucleic acid and peptide sequences
JOURNAL Patent: WO 0229056-A 44 11-APR-2002;
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)

FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 88.5%; Score 1328.8; DB 6; Length 11443;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTCTTTTACAAGACAGTTCTGACAGTGGGAGCGTCTGACCTTTCTCTGCGAAGC 221
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RESULT 7
AX538627

LOCUS AX538627 12057 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 47 from Patent WO0229056.
ACCESSION AX538627
VERSION AX538627.1 GI:25271181

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Chamberlain, J.S. and Harper, S.Q.
TITLE Mini-dystrophin nucleic acid and peptide sequences
JOURNAL Patent: WO 0229056-A 47 11-APR-2002;
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)

FEATURES
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ORIGIN

Query Match		88.5%;	Score 1328.8;	DB 9;	Length 12446;
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RESULT 9
AX409637
LOCUS AX409637 13957 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2284 from Patent WO0229103.
ACCESSION AX409637
VERSION AX409637.1 GI:21442342
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 2284 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
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Query Match 88.5%; Score 1328.8; DB 6; Length 13957;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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RESULT 10
AX538581
LOCUS AX538581 13957 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 1 from Patent WO0229056.
ACCESSION AX538581
VERSION AX538581.1 GI:25271086
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

AUTHORS Chamberlain, J.S. and Harper, S.Q.
TITLE Mini-dystrophin nucleic acid and peptide sequences
JOURNAL Patent: WO 0229056-A 1 11-APR-2002;
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)
FEATURES Location/Qualifiers

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ORIGIN

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Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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RESULT 11

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LOCUS HUMDYS 13957 bp mRNA linear PRI 25-MAY-2000
DEFINITION Homo sapiens dystrophin (DMD) mRNA, complete cds.
ACCESSION M18533 M17154 M18026 M20250
VERSION M18533.1 GI:181856
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1699)
AUTHORS Koenig, M., Hoffman, E.P., Bertelson, C.J., Monaco, A.P., Feener, C. and Kunkel, L.M.
TITLE Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary genomic organization of the DMD gene in normal and affected individuals
JOURNAL Cell 50 (3), 509-517 (1987)
MEDLINE 87273512
PUBMED 3607877
REFERENCE 2 (bases 1678 to 3830)
AUTHORS Hoffman, E.P., Monaco, A.P., Feener, C.C. and Kunkel, L.M.
TITLE Conservation of the Duchenne muscular dystrophy gene in mice and humans
JOURNAL Science 238 (4825), 347-350 (1987)
MEDLINE 88018015
PUBMED 3659917
REFERENCE 3 (bases 1 to 13957)
AUTHORS Koenig, M., Monaco, A.P. and Kunkel, L.M.
TITLE The complete sequence of dystrophin predicts a rod-shaped cytoskeletal protein
JOURNAL Cell 53 (2), 219-226 (1988)
MEDLINE 88194521
PUBMED 3282674
COMMENT On May 25, 2000 this sequence version replaced gi:340693.
Draft entry and computer-readable sequence kindly provided by M.Koenig, 01-APR-1988 The severity of muscular dystrophy is determined by the size of the deleted DNA segment. Deletions found

in different patients were from positions 302-2200, 473-1168, 1691-1810, and 1169-3011.

FEATURES
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ORIGIN

Query Match		88.5%;	Score 1328.8;	DB 9;	Length 13957;
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				Gaps	0;
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QY	222	TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG	281		
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QY	342	CTAAAGAACTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC	401		
Dd	8778	CTAAAGAACTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC	8837		
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QY	1422	ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGGAGGCTGGGCTTCC	1481
Db	9858	ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGGAGGCTGGGCTTCC	9917
QY	1482	TTCTGCATGATTCTATCCAA	1501
Db	9918	TTCTGCATGATTCTATCCAA	9937
RESULT 12			
AR220819			
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DEFINITION	Sequence 60 from patent US 6426186.		
ACCESSION	AR220819		
VERSION	AR220819.1 GI:23327696		
KEYWORDS	Unknown.		
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ORGANISM	Unclassified.		
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AUTHORS	Jones, K.A., Volkmut, W. and Walker, M.G.		
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AF070485

AF070485.1GI:3982750

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1(bases1to13887)

Carville,K.S., Mann,C.J., Schatzberg,S.J. and Wilton,S.D.

Direct Submission

Submitted (04-JUN-1998) ANRI, Pathology, University of Western Australia, Verdun Street, Nedlands, WA 6018, Australia

Location/Qualifiers

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2	1501	100.0	4476	6	AAD37259	100.0	4476	6	AAD37259	100.0	4476	6	AAD37259	100.0	4476	Adeno-ass	
3	1328.8	88.5	2169	6	AAD37232	88.5	2169	6	AAD37232	88.5	2169	6	AAD37232	88.5	2169	Human dys	
4	1328.8	88.5	3531	6	AAD37238	88.5	3531	6	AAD37238	88.5	3531	6	AAD37238	88.5	3531	Human dys	
5	1328.8	88.5	3858	6	AAD37237	88.5	3858	6	AAD37237	88.5	3858	6	AAD37237	88.5	3858	Human dys	
6	1328.8	88.5	3999	6	AAD37234	88.5	3999	6	AAD37234	88.5	3999	6	AAD37234	88.5	3999	Human dys	
7	1328.8	88.5	4182	6	AAD37230	88.5	4182	6	AAD37230	88.5	4182	6	AAD37230	88.5	4182	Human dys	
8	1328.8	88.5	4498	6	AAD37258	88.5	4498	6	AAD37258	88.5	4498	6	AAD37258	88.5	4498	Adeno-ass	
9	1328.8	88.5	4825	6	AAD37257	88.5	4825	6	AAD37257	88.5	4825	6	AAD37257	88.5	4825	Adeno-ass	
10	1328.8	88.5	4848	6	AAD37263	88.5	4848	6	AAD37263	88.5	4848	6	AAD37263	88.5	4848	Adeno-ass	
11	1328.8	88.5	4966	6	AAD37256	88.5	4966	6	AAD37256	88.5	4966	6	AAD37256	88.5	4966	Adeno-ass	
12	1328.8	88.5	4990	6	AAD37262	88.5	4990	6	AAD37262	88.5	4990	6	AAD37262	88.5	4990	Adeno-ass	
13	1328.8	88.5	5060	6	AAD37264	88.5	5060	6	AAD37264	88.5	5060	6	AAD37264	88.5	5060	Adeno-ass	
14	1328.8	88.5	5149	6	AAD37255	88.5	5149	6	AAD37255	88.5	5149	6	AAD37255	88.5	5149	Adeno-ass	
15	1328.8	88.5	5339	6	ABK81998	88.5	5339	6	ABK81998	88.5	5339	6	ABK81998	88.5	5339	DNA encod	
16	1328.8	88.5	5462	6	ABK81999	88.5	5462	6	ABK81999	88.5	5462	6	ABK81999	88.5	5462	DNA encod	
17	1328.8	88.5	5952	5	AAD06794	88.5	5952	5	AAD06794	88.5	5952	5	AAD06794	88.5	5952	Human dys	
18	1328.8	88.5	8689	6	ABK82000	88.5	8689	6	ABK82000	88.5	8689	6	ABK82000	88.5	8689	DNA encod	
19	1328.8	88.5	11058	6	AAD37229	88.5	11058	6	AAD37229	88.5	11058	6	AAD37229	88.5	11058	Human dys	
20	1328.8	88.5	11241	6	ABK82005	88.5	11241	6	ABK82005	88.5	11241	6	ABK82005	88.5	11241	cDNA encod	
21	1328.8	88.5	11443	6	ABK82002	88.5	11443	6	ABK82002	88.5	11443	6	ABK82002	88.5	11443	DNA encod	
22	1328.8	88.5	12923	1	AAN90338	88.5	12923	1	AAN90338	88.5	12923	1	AAN90338	88.5	12923	Sequence	
23	1328.8	88.5	13957	6	ABK81959	88.5	13957	6	ABK81959	88.5	13957	6	ABK81959	88.5	13957	CDNA encod	

24	1328.8	88.5	13957	6	ABT10904	1328.8	88.5	13957	6	ABT10904	1328.8	88.5	13957	6	ABT10904	Human bre
25	1328.8	88.5	13957	6	ABN95786	1328.8	88.5	13957	6	ABN95786	1328.8	88.5	13957	6	ABN95786	Gene #228
26	1328.8	88.5	13957	6	ABS69900	1328.8	88.5	13957	6	ABS69900	1328.8	88.5	13957	6	ABS69900	Human dys
27	1324	88.2	1821	6	AAD37241	1324	88.2	1821	6	AAD37241	1324	88.2	1821	6	AAD37241	Human dys
28	1317.8	87.8	13977	6	ABS70403	1317.8	87.8	13977	6	ABS70403	1317.8	87.8	13977	6	ABS70403	Human bon
29	1149.6	76.6	13815	6	ABK81960	1149.6	76.6	13815	6	ABK81960	1149.6	76.6	13815	6	ABK81960	CDNA enco
30	1149.6	76.6	13815	6	ABI99799	1149.6	76.6	13815	6	ABI99799	1149.6	76.6	13815	6	ABI99799	Mouse isc
31	1149.6	76.6	19307	2	AAT27558	1149.6	76.6	19307	2	AAT27558	1149.6	76.6	19307	2	AAT27558	Shuttle v
32	1148	76.5	13815	2	AAV18885	1148	76.5	13815	2	AAV18885	1148	76.5	13815	2	AAV18885	Mus muscu
33	1041	69.4	3446	6	AAD37242	1041	69.4	3446	6	AAD37242	1041	69.4	3446	6	AAD37242	Human dys
34	1041	69.4	4414	6	AAD37260	1041	69.4	4414	6	AAD37260	1041	69.4	4414	6	AAD37260	Adeno-ass
35	1011.6	67.4	5417	6	ABK81997	1011.6	67.4	5417	6	ABK81997	1011.6	67.4	5417	6	ABK81997	DNA encod
36	1006.2	67.0	4402	3	AAZ48567	1006.2	67.0	4402	3	AAZ48567	1006.2	67.0	4402	3	AAZ48567	A rod sho
37	937	62.4	1434	6	AAD37243	937	62.4	1434	6	AAD37243	937	62.4	1434	6	AAD37243	Human dys
38	807	53.8	4402	3	AAZ48568	807	53.8	4402	3	AAZ48568	807	53.8	4402	3	AAZ48568	A rod sho
39	671.4	44.7	4075	3	AAZ48569	671.4	44.7	4075	3	AAZ48569	671.4	44.7	4075	3	AAZ48569	A rod sho
40	667.2	44.5	3747	3	AAZ48566	667.2	44.5	3747	3	AAZ48566	667.2	44.5	3747	3	AAZ48566	A rod sho
41	613.6	40.9	3163	3	AAZ48571	613.6	40.9	3163	3	AAZ48571	613.6	40.9	3163	3	AAZ48571	A rod sho
42	555.6	37.0	10705	7	ABT41896	555.6	37.0	10705	7	ABT41896	555.6	37.0	10705	7	ABT41896	Toxicity
43	554.2	36.9	11096	6	ABK81962	554.2	36.9	11096	6	ABK81962	554.2	36.9	11096	6	ABK81962	CDNA enco
44	547.4	36.5	6045	2	AAT74665	547.4	36.5	6045	2	AAT74665	547.4	36.5	6045	2	AAT74665	Utrrophin
45	547.4	36.5	6059	4	AAF84673	547.4	36.5	6059	4	AAF84673	547.4	36.5	6059	4	AAF84673	Nucleotid

ALIGNMENTS

RESULT 1		AAD37240		AAD37240 standard; DNA; 3510 BP.	
ID	XX	AC	AD	AA	AA
XX	XX	AC	AD	AA	AA
XX	XX	AC	AD	AA	AA
DT	DT	21-AUG-2002	(first entry)		
XX	XX	Human dystrophin minigene	delta3510.		
DE	DE	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;			
KW	KW	adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;			
KW	KW	Becker muscular dystrophy; ds.			
XX	XX	Homo sapiens.			
OS	OS	WO200183695-A2.			
XX	XX	08-NOV-2001.			
PN	PN	27-APR-2001; 2001WO-US013677.			
XX	XX	28-APR-2000; 2000US-0200777P.			
PF	PF	(XIAO/) XIAO X.			
XX	XX	Xiao X;			
PR	PR	WPI; 2002-049342/06.			
XX	XX	New dystrophin minigene for treating Duchenne or Becker muscular			
PA	PA	dystrophy comprises an N-terminal domain or modified N-terminal domain,			
XX	XX	rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin			
XX	XX	gene.			
XX	XX	Example 1; Page 51-52; 71pp; English.			
XX	XX	The present invention relates to an isolated nucleotide sequence encoding			
CC	CC	a dystrophin minigene. The minigene comprises N-terminal or modified N-			
CC	CC	terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4			
CC	CC	domains and cysteine-rich domains of dystrophin or utrophin genes. The			
CC	CC	invention also relates to a recombinant adeno-associated virus (AAV)			
CC	CC	comprising dystrophin minigene operably linked to an expression control			
CC	CC	element. The dystrophin minigene in operable linkage with an expression			
CC	CC	control element, in a recombinant adeno-associated virus or retrovirus is			
CC	CC	useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular			

CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta3510 containing nucleotides 1-1668 (N-terminus,
CC hinge H1 and rods R2), 8407-10227 (rods R23 and R24, hinge H4 and
CC CR domain) and 11047-11058 (dystrophin last 3 amino acids)
XX
SQ Sequence 3510 BP; 1073 A; 787 C; 828 G; 822 T; 0 U; 0 Other;

Query Match 100.0%; Score 1501; DB 6; Length 3510;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGATCTAGAACAAAGCAAGTCAGGGTCAATTCTCTCACTCACATGGTGGTGGTAGT 60
DB |||||
1500 AGAAGATCTAGAACAAAGCAAGTCAGGGTCAATTCTCTCACTCACATGGTGGTGGTAGT 1559
QY 61 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 120
DB |||||
1560 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 1619
QY 121 AGATCGATGGCAAAACATCTGTAGATGGACAGAACCGCTGGGTCTTTTACAAGACAG 180
DB |||||
1620 AGATCGATGGCAAAACATCTGTAGATGGACAGAACCGCTGGGTCTTTTACAAGACAG 1679
QY 181 TTCTGACCAAGTGAAGCGCTCTGCACCTTTCTCTGCAGGAACCTTCTGGTGTGGCTACAGCT 240
DB |||||
1680 TTCTGACCAAGTGAAGCGCTCTGCACCTTTCTCTGCAGGAACCTTCTGGTGTGGCTACAGCT 1739
QY 241 GAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCAGAGCAGTTTCAGAA 300
DB |||||
1740 GAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCAGAGCAGTTTCAGAA 1799
QY 301 GCAGAACGATGACATAGGGCCTTCAAGAGGGAATTGAAAACTTAAAGAACCTGTATCAT 360
DB |||||
1800 GCAGAACGATGACATAGGGCCTTCAAGAGGGAATTGAAAACTTAAAGAACCTGTATCAT 1859
QY 361 GAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCCTTTGGAAGGACTAGAGAA 420
DB |||||
1860 GAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCCTTTGGAAGGACTAGAGAA 1919
QY 421 ACTTACAGGAGCCAGAGAGCTGCTCTCTGAGGAGAGAGCCAGAAATGTCACTCGGCT 480
DB |||||
1920 ACTTACAGGAGCCAGAGAGCTGCTCTCTGAGGAGAGAGCCAGAAATGTCACTCGGCT 1979
QY 481 TCTACGAAAGAGCTGAGGAGGTCAATACTAGTGGGAAATTAAGAACCTGCACCTCCGC 540
DB |||||
1980 TCTACGAAAGAGCTGAGGAGGTCAATACTAGTGGGAAATTAAGAACCTGCACCTCCGC 2039
QY 541 TGACTGGCAGAGAAAAATAGATGAGACCTTGAAGACTCCAGAACTTCAAGAGGCGCAC 600
DB |||||
2040 TGACTGGCAGAGAAAAATAGATGAGACCTTGAAGACTCCAGAACTTCAAGAGGCGCAC 2099
QY 601 GGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGATCAAGGGATCCTGGCAGCCGT 660
DB |||||
2100 GGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGATCAAGGGATCCTGGCAGCCGT 2159
QY 661 GGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGG 720
DB |||||
2160 GGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGG 2219
QY 721 AGAAATTGCGCTCTGAAAGAGAACGCTGAGCCACGCTCAATGACCTTGCTCGCCAGCTTAC 780
DB |||||
2220 AGAAATTGCGCTCTGAAAGAGAACGCTGAGCCACGCTCAATGACCTTGCTCGCCAGCTTAC 2279
QY 781 CACTTTGGGCATTGAGCTCTCACCGTATACCTCAGCACTCTGGAAGACCTGAACACACAG 840
DB |||||
2280 CACTTTGGGCATTGAGCTCTCACCGTATACCTCAGCACTCTGGAAGACCTGAACACACAG 2339
QY 841 ATGGAAGCTTCTGAGGTTGGCCGTCGAGGACCGAGTCAGGCACTGCATGAAGCCACAG 900
DB |||||
2340 ATGGAAGCTTCTGAGGTTGGCCGTCGAGGACCGAGTCAGGCACTGCATGAAGCCACAG 2399
QY 901 GGACTTTGGTCCAGCATCTCAGCACTTCTTCCACGCTCTTCCAGGGTCCCTGGGAGAG 960
DB |||||

Db 2400. GGACTTTGGTCCAGCATCTCAGCACTTTTCTTCCAGCTCTGTCCAGGGTCCCTGGGAGAG 2459
QY 961 AGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCAGAGACTCAAAACAACCTTGCTG 1020
DB |||||
2460 AGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCAGAGACTCAAAACAACCTTGCTG 2519
QY 1021 GGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGCTGACCTGAATAATGTGAGATT 1080
DB |||||
2520 GGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGCTGACCTGAATAATGTGAGATT 2579
QY 1081 CTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAGGCCCTTTGCTTGGATCT 1140
DB |||||
2580 CTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAGGCCCTTTGCTTGGATCT 2639
QY 1141 CTTGAGCCTGTGAGCTGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB |||||
2640 CTTGAGCCTGTGAGCTGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2699
QY 1201 GCCCATGGATATCCTGCAGATTATTAAATTGTTTGACCACTATTATGACCGCCTGGAGCA 1260
DB |||||
2700 GCCCATGGATATCCTGCAGATTATTAAATTGTTTGACCACTATTATGACCGCCTGGAGCA 2759
QY 1261 AGAGCACAAATTTGGTCAACGTCCTCTCTCGTGGATATGTGTCTGAACTGGCTGCT 1320
DB |||||
2760 AGAGCACAAATTTGGTCAACGTCCTCTCTCGTGGATATGTGTCTGAACTGGCTGCT 2819
QY 1321 GAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGCTTTTAAAACTGGCAT 1380
DB |||||
2820 GAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGCTTTTAAAACTGGCAT 2879
QY 1381 CATTTCCCTGTGTAAGACACATTTGGAAGACAAAGTACAGATACCTTTCAAGCAAGTGGC 1440
DB |||||
2880 CATTTCCCTGTGTAAGACACATTTGGAAGACAAAGTACAGATACCTTTCAAGCAAGTGGC 2939
QY 1441 AAGTTCAACAGGATTTTGTGACCGAGCGAGGCTGGGCTCCTTCTGATGATTTCTATCCA 1500
DB |||||
2940 AAGTTCAACAGGATTTTGTGACCGAGCGAGGCTGGGCTCCTTCTGATGATTTCTATCCA 2999
QY 1501 A 1501
DB 3000 A 3000

RESULT 2
AAD37259
ID AAD37259 standard; DNA; 4476 BP.
XX AAD37259;
AC AAD37259;
XX 21-AUG-2002 (first entry)
DT 21-AUG-2002 (first entry)
XX Adeno-associated virus vector plasmid, AAV-MCK-3510.
DE Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
XX adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX Homo sapiens.
OS Unidentified.
OS Chimeric.
XX WO200183695-A2.
PN 08-NOV-2001.
XX 27-APR-2001; 2001WO-US013677.
PF 28-APR-2000; 2000US-0200777P.
XX (XIAO/) XIAO X.
PA XIAO X;
XX

KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
XX

PN WO200183695-A2.

XX 08-NOV-2001.

PF 27-APR-2001; 2001WO-US013677.

XX 28-APR-2000; 2000US-0200777P.

PA (XIAO/) XIAO X.

XX Xiao X;

DR WPI; 2002-049342/06.

XX New dystrophin minigene for treating Duchenne or Becker muscular

PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX

PS Example 1; Page 50-51; 71pp; English.

XX The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta3531 containing nucleotides 1-1341 (N-terminus,
CC hinge H1 and rod R1), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR
CC domain) and 11047-11058 (dystrophin last 3 amino acids)
XX

SQ Sequence 3531 BP; 1071 A; 809 C; 824 G; 827 T; 0 U; 0 Other;

Query Match 88.5%; Score 1328.8; DB 6; Length 3531;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAGTGAAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db |||||
1682 GGTCCCATTTTGAAGCCAGTTCTGACCAGTGAAGCGTCTGCACCTTTCTCTGCAGGAAC 1741

QY 222 TTCTGGTGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281
Db |||||
1742 TTCTGGTGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 1801

QY 282 ACTTTCCAGCAGTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 341
Db |||||
1802 ACTTTCCAGCAGTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 1861

QY 342 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db |||||
1862 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 1921

QY 402 CTTTGGAGGACTAGAGAACTCTACAGGAGGCCAGAGAGCTGCCTCCTCAGGAGAGAG 461
Db |||||
1922 CTTTGGAGGACTAGAGAACTCTACAGGAGGCCAGAGAGCTGCCTCCTCAGGAGAGAG 1981

QY 462 CCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db |||||
1982 CCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 2041

QY 522 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 581
|||

Db 2042 AATTGAACCTGCACCTCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 2101
QY 582 AGGAACTTCAAGAGGCCACCGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 641
Db |||||
2102 AGGAACTTCAAGAGGCCACCGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 2161
QY 642 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 701
Db |||||
2162 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 2221
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAAGAGAACGTTGAGCCACGTC 761
Db |||||
2222 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAAGAGAACGTTGAGCCACGTC 2281
QY 762 ACCTTGCTCGCCAGCTTTACCACTTTGGGCATTTACCGTCTCACCGTATAACCTCAGCACTC 821
Db |||||
2282 ACCTTGCTCGCCAGCTTTACCACTTTGGGCATTTACCGTCTCACCGTATAACCTCAGCACTC 2341
QY 822 TGAAGACCTGAAACACCAAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCCGAGTCAGGC 881
Db |||||
2342 TGAAGACCTGAAACACCAAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCCGAGTCAGGC 2401
QY 882 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCGTG 941
Db |||||
2402 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCGTG 2461
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCCAG 1001
Db |||||
2462 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCCAG 2521
QY 1002 AGACTCAAAACAACTTGTCTGGACCAATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 1061
Db |||||
2522 AGACTCAAAACAACTTGTCTGGACCAATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 2581
QY 1062 ACCTGAATAATGTGAGTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db |||||
2582 ACCTGAATAATGTGAGTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 2641
QY 1122 AGGCGCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGAGTGCATGTCCTTGGACGACACA 1181
Db |||||
2642 AGGCGCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGAGTGCATGTCCTTGGACGACACA 2701
QY 1182 ACCTCAAGCAAAATGACCAAGCCATGGATATCTTGAGATTTAATTTGTTGACCACTA 1241
Db |||||
2702 ACCTCAAGCAAAATGACCAAGCCATGGATATCTCTGAGATTTAATTTGTTGACCACTA 2761
QY 1242 TTTATGACCGCCTGGAGCAAGAGACACAACAATTTGFTCAACGTCCTCTCTGCGTGGATA 1301
Db |||||
2762 TTTATGACCGCCTGGAGCAAGAGACACAACAATTTGFTCAACGTCCTCTCTGCGTGGATA 2821
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTTGCC 1361
Db |||||
2822 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTTGCC 2881
QY 1362 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAGAT 1421
Db |||||
2882 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAGTACAGAT 2941
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGGCTGGGCTCC 1481
Db |||||
2942 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGGCTGGGCTCC 3001
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db |||||
3002 TTCTGCATGATTCTATCCAA 3021

RESULT 5

AAD37237

ID AAD37237 standard; DNA; 3858 BP.

XX

AC AAD37237;

XX

DT	21-AUG-2002 (first entry)	
XX	Human dystrophin minigene delta3849.	
XX	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;	
KW	adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;	
KW	Becker muscular dystrophy; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200183695-A2.	
XX		
PD	08-NOV-2001.	
XX		
PF	27-APR-2001; 2001WO-US013677.	
XX		
PR	28-APR-2000; 2000US-0200777P.	
XX		
PA	(XIAO/) XIAO X.	
PI		
XX	Xiao X;	
XX		
DR	WPI; 2002-049342/06.	
XX		
PT	New dystrophin minigene for treating Duchenne or Becker muscular	
PT	dystrophy comprises an N-terminal domain or modified N-terminal domain,	
PT	rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin	
PT	gene.	
XX		
PS	Example 1; Page 48-49; 71pp; English.	
XX		
CC	The present invention relates to an isolated nucleotide sequence encoding	
CC	a dystrophin minigene. The minigene comprises N-terminal or modified N-	
CC	terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4	
CC	domains and cysteine-rich domains of dystrophin or utrophin genes. The	
CC	invention also relates to a recombinant adeno-associated virus (AAV)	
CC	comprising dystrophin minigene operably linked to an expression control	
CC	element. The dystrophin minigene in operable linkage with an expression	
CC	control element, in a recombinant adeno-associated virus or retrovirus is	
CC	useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular	
CC	dystrophy (BMD) in a mammalian subject. The present sequence is human	
CC	dystrophin minigene delta3849 containing nucleotides 1-1668 (N-terminus,	
CC	hinge H1 and rods R1, R2), 8059-10227 (rods R22, R23 and R24, hinge H4	
CC	and CR domain) and 11047-11058 (dystrophin last 3 amino acids)	
XX		
SQ	Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 U; 0 Other;	
	Query Match 88.5%; Score 1328.8; DB 6; Length 3858;	
	Best Local Similarity 99.5%; Pred. No. 0;	
	Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
QY	162 GGGTTCTTTTACAAGACAGTCTCTGACCAGTGGAGCGTCTGCACCTTTCTCTCGAGGAAC 221	
Db	2009 GGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTCGAGGAAC 2068	
QY	222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCGCGCAGGCACCTATTGGAGCG 281	
Db	2069 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCGCGCAGGCACCTATTGGAGCG 2128	
QY	282 ACTTTCAGCAGTTCCAGAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAAAA 341	
Db	2129 ACTTTCAGCAGTTCCAGAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAAAA 2188	
QY	342 CTAAGAAGCCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401	
Db	2189 CTAAGAAGCCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 2248	
QY	402 CTTTGGAGGACTAGAGAAACTCTACCAGGAGCCCAAGAGAGCTGCCCTCCTGAGGAGAG 461	
Db	2249 CTTTGGAGGACTAGAGAAACTCTACCAGGAGCCCAAGAGAGCTGCCCTCCTGAGGAGAG 2308	
QY	462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAA 521	

ID AAD37234 standard; DNA; 3999 BP.
XX
AC AAD37234;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human dystrophin minigene delta3990.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
XX
XX WO200183695-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 27-APR-2001; 2001WO-US013677.
PF
XX
XX 28-APR-2000; 2000US-020077P.
PR
XX
XX (XIAO/) XIAO X.
PA
XX
XX Xiao X;
PI
XX
XX WPI; 2002-049342/06.
DR
XX
XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
XX Example 1; Page 46-47; 71pp; English.
PS
XX
XX The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta3990 containing nucleotides 1-1668 (N-terminus,
CC hinge H1 and rods R1 and R2), 8059-10227 (rods R22, R23 and R24, hinge H4
CC and CR domain) and 11047-11058 (dystrophin last 3 amino acids)
XX
SQ Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 U; 0 Other;
Query Match 88.5%; Score 1328.8; DB 6; Length 3999;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 162 GGGTCTTTTACAAGACAGTTCTGACCAGTGAAGCGTCTGCACCTTTCTCTGCAGGAAC 221
DB |||||
QY 222 TTCTGGTGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGCG 281
DB |||||
QY 2210 TTCTGGTGTGGCTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGCG 2269
DB |||||
QY 282 ACTTCCAGCAGTTTCAGAAGCAGAACGATGTACATAGGCCCTTCAAGAGGGAATTGAAAA 341
DB |||||
QY 2270 ACTTCCAGCAGTTTCAGAAGCAGAACGATGTACATAGGCCCTTCAAGAGGGAATTGAAAA 2329
DB |||||
QY 342 CTAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
DB |||||
QY 2330 CTAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 2389
DB |||||
QY 402 CTTTGGAGGACTAGAGAACTCTACAGGAGGCCAGAGAGCTGCCTCCTGAGGAGAGAG 461
DB |||||

Db 2390 CTTTGGAAGGACTAGAGAAAACTCTACCAGGAGGCCAGAGAGCTGCCTCCTGAGGAGAGAG 2449
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
XX |||||
Db 2450 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 2509
XX |||||
QY 522 AATTGAACCTGCACCTCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 581
XX |||||
Db 2510 AATTGAACCTGCACCTCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 2569
XX |||||
QY 582 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 641
XX |||||
Db 2570 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 2629
XX |||||
QY 642 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 701
XX |||||
Db 2630 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 2689
XX |||||
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACTGTAGCCCACTCAATG 761
XX |||||
Db 2690 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACTGTAGCCCACTCAATG 2749
XX |||||
QY 762 ACCTTGCTCGCCAGCTTACCACTTTTGGGCATTACGCTCTCACCGTATAAACCCTCAGCACTC 821
XX |||||
Db 2750 ACCTTGCTCGCCAGCTTACCACTTTTGGGCATTACGCTCTCACCGTATAAACCCTCAGCACTC 2809
XX |||||
QY 822 TGGAAAGACCTGAACACCAAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAGGC 881
XX |||||
Db 2810 TGGAAAGACCTGAACACCAAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAGGC 2869
XX |||||
QY 882 AGTGCATGAAGCCCAAGGACTTTGGTCCAGCATCTCTCAGCACTTCTTTTCCACGTCTG 941
XX |||||
Db 2870 AGTGCATGAAGCCCAAGGACTTTGGTCCAGCATCTCTCAGCACTTCTTTCCACGTCTG 2929
XX |||||
QY 942 TCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAAGTGCCTTACTATATCAACCACG 1001
XX |||||
Db 2930 TCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAAGTGCCTTACTATATCAACCACG 2989
XX |||||
QY 1002 AGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 1061
XX |||||
Db 2990 AGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 3049
XX |||||
QY 1062 ACCTGAATAATGTGAGATCTCAGATTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
XX |||||
Db 3050 ACCTGAATAATGTGAGATTCAGATTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3109
XX |||||
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCGATGTGATGCCTTGGACCCAGCACA 1181
XX |||||
Db 3110 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCGATGTGATGCCTTGGACCCAGCACA 3169
XX |||||
QY 1182 ACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAAGATTATTAAATTTGTGACCACTA 1241
XX |||||
Db 3170 ACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAAGATTATTAAATTTGTGACCACTA 3229
XX |||||
QY 1242 TTTATGACCGCCTGGAGCAAGACACAACAATTTGGTCAACGTCCTCTCTGCGTGGATA 1301
XX |||||
Db 3230 TTTATGACCGCCTGGAGCAAGACACAACAATTTGGTCAACGTCCTCTCTGCGTGGATA 3289
XX |||||
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 1361
XX |||||
Db 3290 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 3349
XX |||||
QY 1362 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGACATTTTGAAGACAAGTACAGAT 1421
XX |||||
Db 3350 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGACATTTTGAAGACAAGTACAGAT 3409
XX |||||
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTACCGCAGGCTGGGCCTCC 1481
XX |||||
Db 3410 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTACCGCAGGCTGGGCCTCC 3469
XX |||||
QY 1482 TTCTGCATGATTCTATCCAA 1501
XX |||||
Db 3470 TTCTGCATGATTCTATCCAA 3489
XX |||||

RESULT 7
AAD37230
ID AAD37230 standard; DNA; 4182 BP.
XX
AC AAD37230;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human dystrophin minigene delta4173.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX
XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 43-44; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta4173 containing nucleotides 1-1992 (N-terminus,
CC hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R24,
CC hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids)
XX
SQ Sequence 4182 BP; 1309 A; 927 C; 970 G; 976 T; 0 U; 0 Other;

Query Match 88.5%; Score 1328.8; DB 6; Length 4182;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGAAC 221
DB 2333 GGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGAAC 2392

QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCCGCAGGCACCTATTGGAGGCG 281
DB 2393 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCCGCAGGCACCTATTGGAGGCG 2452

QY 282 ACTTTCCAGCAGTTTCAGAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAAAA 341
DB 2453 ACTTTCCAGCAGTTTCAGAAGCAGAACGATGTACATAGGCGCTTCAAGAGGGAATTGAAAA 2512

QY 342 CTAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
DB 342 CTAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401

Db 2513 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 2572
QY 402 CTTTGGGAAGGACTAGAGAAACTCTACCCAGGAGCCAGAGAGCTGCTCTCTGAGGAGAGAG 461
DB 2573 CTTTGGGAAGGACTAGAGAAACTCTACCCAGGAGCCAGAGAGCTGCTCTCTGAGGAGAGAG 2632
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
DB 2633 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 2692
QY 522 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 581
DB 2693 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 2752
QY 582 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 641
DB 2753 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 2812
QY 642 AGGATCCTGGCAGCCCGTGGCGGATCTCTCTCATTTGACTCTCTCCAAGATCACCTCGAGA 701
DB 2813 AGGATCCTGGCAGCCCGTGGCGGATCTCTCTCATTTGACTCTCTCCAAGATCACCTCGAGA 2872
QY 702 AAGTCAAGGCACTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACGTGAGCCACGTCAATG 761
DB 2873 AAGTCAAGGCACTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACGTGAGCCACGTCAATG 2932
QY 762 ACCTTGCTCGCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 821
DB 2933 ACCTTGCTCGCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 2992
QY 822 TGAAGACCTTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 881
DB 2993 TGAAGACCTTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 3052
QY 882 AGCTGCATGAAGCCCAACAGGCACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGCTGTG 941
DB 3053 AGCTGCATGAAGCCCAACAGGCACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGCTGTG 3112
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACACAG 1001
DB 3113 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACACAG 3172
QY 1002 AGACTCAAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTTACCAGTCTTTAGCTG 1061
DB 3173 AGACTCAAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTTACCAGTCTTTAGCTG 3232
QY 1062 ACCTGAATAATGTGAGATTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
DB 3233 ACCTGAATAATGTGAGATTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3292
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCAATGATGCCTTGGACCAGACA 1181
DB 3293 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCAATGATGCCTTGGACCAGACA 3352
QY 1182 ACCTCAAGCAAAATGACCCCATGGATATCCTGCAGATTAATTAATTGTTTGACCACTA 1241
DB 3353 ACCTCAAGCAAAATGACCCCATGGATATCCTGCAGATTAATTAATTGTTTGACCACTA 3412
QY 1242 TTTATGACCGCCTGGAGCAAGAGACACAACAATTTGGTCAACGTCCTCTCTCGGTGGATA 1301
DB 3413 TTTATGACCGCCTGGAGCAAGAGACACAACAATTTGGTCAACGTCCTCTCTCGGTGGATA 3472
QY 1302 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 1361
DB 3473 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 3532
QY 1362 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAGTACAGAT 1421
DB 3533 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAGTACAGAT 3592
QY 1422 ACCTTTTCAAGCAAGTGGCAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCTTCC 1481
DB 3593 ACCTTTTCAAGCAAGTGGCAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCTTCC 3652

QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 3653 TTCTGCATGATTCTATCCAA 3672

RESULT 8

AAD37258
ID AAD37258 standard; DNA; 4498 BP.
XX
AC AAD37258;
XX
DT 21-AUG-2002 (first entry)
XX
DE Adeno-associated virus vector plasmid, AAV-MCK-3531.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.

XX Homo sapiens.
OS Unidentified.
OS Chimeric.

XX WO200183695-A2.

XX 08-NOV-2001.

XX 27-APR-2001; 2001WO-US013677.

XX 28-APR-2000; 2000US-0200777P.

XX (XIAO/) XIAO X.

XX Xiao X;

XX WPI; 2002-049342/06.

XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.

XX Example 1; Page 62-63; 71pp; English.

XX The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence

XX Sequence 4498 BP; 1251 A; 1118 C; 1123 G; 1006 T; 0 U; 0 Other;

SQ Query Match 88.5%; Score 1328.8; DB 6; Length 4498;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTCTTGACCCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAAC 221

Db 2439 GGTCCCATTTTGAAGCCAGTTCTTGACCCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAAC 2498

QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281

Db 2499 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 2558

QY 282 ACTTCCAGCAGTTCAGAACAGAACGATGTACATAGGCCCTTCAAGAGGGAATTGAAA 341

Db 2559 ACTTCCAGCAGTTCAGAACAGAACGATGTACATAGGCCCTTCAAGAGGGAATTGAAA 2618
QY 342 CTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 2619 CTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 2678
QY 402 CTTTGGAGGACTAGAGAAACTCTACCAGGAGGCCACAGAGAGTGCCTCCTGAGGAGAGAG 461
Db 2679 CTTTGGAGGACTAGAGAAACTCTACCAGGAGGCCACAGAGAGTGCCTCCTGAGGAGAGAG 2738
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 2739 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 2798
QY 522 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAGAAATAAGATGAGACCCCTTGAAAGACTCC 581
Db 2799 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAGAAATAAGATGAGACCCCTTGAAAGACTCC 2858
QY 582 AGGAACTTCAAGAGGCCACGGAATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 641
Db 2859 AGGAACTTCAAGAGGCCACGGAATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 2918
QY 642 AGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 701
Db 2919 AGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 2978
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAACGTTGAGCCACGTCAAATG 761
Db 2979 AAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAACGTTGAGCCACGTCAAATG 3038
QY 762 ACCTTGCTCGCCAGCTTACCACTTTGGGCATTTGAGCTCTCACCGTATAACCTCAGCACTC 821
Db 3039 ACCTTGCTCGCCAGCTTACCACTTTGGGCATTTGAGCTCTCACCGTATAACCTCAGCACTC 3098
QY 822 TGAAGACCTGAACACACCCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 881
Db 3099 TGAAGACCTGAACACACCCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 3158
QY 882 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCAGCTCTG 941
Db 3159 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCAGCTCTG 3218
QY 942 TCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCCAACAAAGTGCCTACTATATCAACCACG 1001
Db 3219 TCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCCAACAAAGTGCCTACTATATCAACCACG 3278
QY 1002 AGACTCAAAACAACTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 1061
Db 3279 AGACTCAAAACAACTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 3338
QY 1062 ACCTGAATAATGTCAAGTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3339 ACCTGAATAATGTCAAGTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3398
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGAGTGCATGTGATGCCCTTGGACGACACA 1181
Db 3399 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCCTGTGAGTGCATGTGATGCCCTTGGACGACACA 3458
QY 1182 ACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTA 1241
Db 3459 ACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTA 3518
QY 1242 TTTATGACCGCCTGGAGCAAGAGCACAACAATTTGTGTCACAGTCCCTCTCTCGCTGGATA 1301
Db 3519 TTTATGACCGCCTGGAGCAAGAGCACAACAATTTGTGTCACAGTCCCTCTCTCGCTGGATA 3578
QY 1302 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCCGTGTCC 1361
Db 3579 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCCGTGTCC 3638
QY 1362 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAGTACAGAT 1421

Db 3639 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGGAAAGACAAAGTACAGAT 3698
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGGCGCAGGCTGGGCTTCC 1481
Db 3699 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGGCGCAGGCTGGGCTTCC 3758
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 3759 TTCTGCATGATTCTATCCAA 3778

RESULT 9

AAD37257
ID AAD37257 standard; DNA; 4825 BP.

XX AAD37257;

XX 21-AUG-2002 (first entry)

DE Adeno-associated virus vector plasmid, AAV-MCK-delta3849.

XX Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.

OS Homo sapiens.
OS Unidentified.
OS Chimeric.

XX WO200183695-A2.

XX 08-NOV-2001.

XX 27-APR-2001; 2001WO-US013677.

XX 28-APR-2000; 2000US-0200777P.

XX (XIAO/) XIAO X.

XX Xiao X;

XX WPI; 2002-049342/06.

XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.

XX Example 1; Page 61-62; 71pp; English.

PS The present invention relates to an isolated nucleotide sequence encoding
XX a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence

XX Sequence 4825 BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 U; 0 Other;

XX Query Match 88.5%; Score 1328.8; DB 6; Length 4825;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGAAC 221

Db 2766 GGTCCCATTTGGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGAAC 2825

QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281
Db 2826 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 2885
QY 282 ACTTTCCAGCAGTTTCAAGACAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTTGAAA 341
Db 2886 ACTTTCCAGCAGTTTCAAGACAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTTGAAA 2945
QY 342 CTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 2946 CTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 3005
QY 402 CTTTGGAGGACTAGAGAAACTCTACAGGAGCCCGAGAGCTGCTCCTGAGGAGAGAG 461
Db 3006 CTTTGGAGGACTAGAGAAACTCTACAGGAGCCCGAGAGCTGCTCCTGAGGAGAGAG 3065
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 3066 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 3125
QY 522 AATTGAACCTGCACCTCCGCTGACTGCGAGAGAAAATAGATGAGACCCCTTGAAGACTCC 581
Db 3126 AATTGAACCTGCACCTCCGCTGACTGCGAGAGAAAATAGATGAGACCCCTTGAAGACTCC 3185
QY 582 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 641
Db 3186 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 3245
QY 642 AGGGATCCTGCGCAGCCCGTGGCGGATCTCTCATTTGACTCTCTCCTCAAGATCACCTCGAGA 701
Db 3246 AGGGATCCTGCGCAGCCCGTGGCGGATCTCTCATTTGACTCTCTCCTCAAGATCACCTCGAGA 3305
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCCCTCTGAAAGAGAACGCTGAGCCACGTCATG 761
Db 3306 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCCCTCTGAAAGAGAACGCTGAGCCACGTCATG 3365
QY 762 ACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATTAACCTCAGCACTC 821
Db 3366 ACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATTAACCTCAGCACTC 3425
QY 822 TGAAGACCTGAACACCAAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAGGC 881
Db 3426 TGAAGACCTGAACACCAAGATGGAAGCTTCTGAGGTGGCCGTCGAGGACCGAGTCAGGC 3485
QY 882 AGCTGCATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCG 941
Db 3486 AGCTGCATGAAGCCCAACAGGACCTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCG 3545
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACACG 1001
Db 3546 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACACG 3605
QY 1002 AGACTCAAAACAACCTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGCTG 1061
Db 3606 AGACTCAAAACAACCTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGTCTTTAGCTG 3665
QY 1062 ACCTGAATATATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3666 ACCTGAATATATGTGAGATTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3725
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGTCATGTGATGCTTGGACCAGCACA 1181
Db 3726 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGTCATGTGATGCTTGGACCAGCACA 3785
QY 1182 ACCTCAAGCAAAAATGACCAAGCCCATGGATATCCTGCAGATTTAATTGTTTGACCACTA 1241
Db 3786 ACCTCAAGCAAAAATGACCAAGCCCATGGATATCCTGCAGATTTAATTGTTTGACCACTA 3845
QY 1242 TTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTCGGTGGATA 1301
Db 3846 TTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTCGGTGGATA 3905
QY 1302 TGTGTCTGAAGTGGCTGTCTGAATGTATTATGATACGGGACGAACAGGGAGGATCCGTGTCC 1361

Db 3906 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGTCC 3965
QY 1362 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGAT 1421
Db 3966 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGAT 4025
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTCC 1481
Db 4026 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTCC 4085
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 4086 TTCTGCATGATTCTATCCAA 4105

RESULT 10
AAD37263
ID AAD37263 standard; DNA; 4848 BP.

AC AAD37263;

XX 21-AUG-2002 (first entry)

DE Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849.

XX Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.

OS Homo sapiens.
OS Cytomegalovirus.
OS Unidentified.
OS Chimeric.

XX WO200183695-A2.

PN 08-NOV-2001.

XX 27-APR-2001; 2001WO-US013677.

PR 28-APR-2000; 2000US-0200777P.

XX (XIAO/) XIAO X.

PI Xiao X;

XX WPI; 2002-049342/06.

DR New dystrophin minigene for treating Duchenne or Becker muscular
XX dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.

XX Example 1; Page 68-70; 71pp; English.

CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a
CC cytomegalovirus (CMV) promoter and a small polyA signal sequence

XX Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 U; 0 Other;

Query Match 88.5%; Score 1328.8; DB 6; Length 4848;
Best Local Similarity 99.5%; Pred. No. 0;

Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 162 GGGTTCTTTTACAGACAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGAAC 221
Db 2789 GGTCCATTGGAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGAAC 2848
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTTATTGGAGCG 281
Db 2849 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTTATTGGAGCG 2908
QY 282 ACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 341
Db 2909 ACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 2968
QY 342 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTTGACAGAGCAGC 401
Db 2969 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTTGACAGAGCAGC 3028
QY 402 CTTTGGAAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCTCTGAGGAGAG 461
Db 3029 CTTTGGAAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCTCTGAGGAGAG 3088
QY 462 CCCAGAAATGTCACCTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAA 521
Db 3089 CCCAGAAATGTCACCTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAA 3148
QY 522 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 581
Db 3149 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 3208
QY 582 AGGAACCTTCAAGAGGCCACCGATGAGTGGACCTCAAGCTCGGCCAAGCTGAGGTGATCA 641
Db 3209 AGGAACCTTCAAGAGGCCACCGATGAGTGGACCTCAAGCTCGGCCAAGCTGAGGTGATCA 3268
QY 642 AGGATCCTTGGCAGCCCGTGGCGATCTCTCAATTGACTCTCTCCAAGATCACCTCGAGA 701
Db 3269 AGGATCCTTGGCAGCCCGTGGCGATCTCTCAATTGACTCTCTCCAAGATCACCTCGAGA 3328
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACCTGAGCCACGTCATG 761
Db 3329 AAGTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACCTGAGCCACGTCATG 3388
QY 762 ACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 821
Db 3389 ACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 3448
QY 822 TGGAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 881
Db 3449 TGGAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 3508
QY 882 AGTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCTG 941
Db 3509 AGTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCTG 3568
QY 942 TCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCAAACAAAGTCCCTACTATATCAACCACG 1001
Db 3569 TCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCAAACAAAGTCCCTACTATATCAACCACG 3628
QY 1002 AGACTCAAAACAACCTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 1061
Db 3629 AGACTCAAAACAACCTTGTCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 3688
QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3689 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3748
QY 1122 AGGCCCTTTGCTTGGATCTCTTGGCCCTGTGAGCTGCATGTGATGCCCTTGGACCAGCACA 1181
Db 3749 AGGCCCTTTGCTTGGATCTCTTGGCCCTGTGAGCTGCATGTGATGCCCTTGGACCAGCACA 3808
QY 1182 ACCTCAAGCAAAATGACCAGCCCATGGATATCCTGAGATTATTAATTGTTGACCACTA 1241
Db 3809 ACCTCAAGCAAAATGACCAGCCCATGGATATCCTGAGATTATTAATTGTTGACCACTA 3868

QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGA 1121
Db 3831 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGA 3890
QY 1122 AGGCCCTTTGCTGGATCTCTTGAGCCTGTGAGCTGCTGATGATGCTTGGACCAAGACA 1181
Db 3891 AGGCCCTTTGCTGGATCTCTTGAGCCTGTGAGCTGCTGATGATGCTTGGACCAAGACA 3950
QY 1182 ACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCACTA 1241
Db 3951 ACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCACTA 4010
QY 1242 TTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATA 1301
Db 4011 TTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATA 4070
QY 1302 TGTGCTGAACCTGCTGCTGAATGTTTATGATACGGGACGACAGGAGGATCCGTGTCC 1361
Db 4071 TGTGCTGAACCTGCTGCTGAATGTTTATGATACGGGACGACAGGAGGATCCGTGTCC 4130
QY 1362 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAAGTACAGAT 1421
Db 4131 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAAGTACAGAT 4190
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGAGGCTGGGCTCC 1481
Db 4191 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCGAGGCTGGGCTCC 4250
QY 1482 TTCTGCATGATTTCTATCCAA 1501
Db 4251 TTCTGCATGATTTCTATCCAA 4270

RESULT 13

AAD37264
ID AAD37264 standard; DNA; 5060 BP.
XX
AC AAD37264;
XX
DT 21-AUG-2002 (first entry)
XX
DE Adeno-associated virus (AAV) vector plasmid, AAV-E-CMV-3849.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
OS Cytomegalovirus.
OS Unidentified.
OS Chimeric.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI xiao X;
XX
DR WPI; 2002-049342/06.
XX
PT New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 70-71; 71pp; English.
XX

CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) enhancer, a cytomegalovirus (CMV) promoter and a
CC small polyA signal sequence
XX
SQ Sequence 5060 BP; 1449 A; 1217 C; 1234 G; 1160 T; 0 U; 0 Other;
Query Match 88.5%; Score 1328.8; DB 6; Length 5060;
Best Local Similarity 99.5%; Pred.No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db 3001 GGTCCCATTTTGAAGCCAGTTCTGACCAAGTGAAGCGTCTGCACCTTTCTCTGCAGGAAC 3060
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGGACACCTATTGGAGGCG 281
Db 3061 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGGACACCTATTGGAGGCG 3120
QY 282 ACTTTCCAGCAGTTTCAAGACAGAACGATGTATGATGATTAAGCCGCGGACACCTATTGAAA 341
Db 3121 ACTTTCCAGCAGTTTCAAGACAGAACGATGTATGATGATTAAGCCGCGGACACCTATTGAAA 3180
QY 342 CTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 3181 CTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCAGC 3240
QY 402 CTTTGGAGGACTAGAGAACTCTACCCAGGAGCCAGAGAGCTGCTCTCTGAGGAGAGAG 461
Db 3241 CTTTGGAGGACTAGAGAACTCTACCCAGGAGCCAGAGAGCTGCTCTCTGAGGAGAGAG 3300
QY 462 CCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 3301 CCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 3360
QY 522 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAGAAAAATAGATGAGACCTTGAAGACTCC 581
Db 3361 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAGAAAAATAGATGAGACCTTGAAGACTCC 3420
QY 582 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGATCA 641
Db 3421 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGATCA 3480
QY 642 AGGATCCTTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGA 701
Db 3481 AGGATCCTTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGA 3540
QY 702 AAGTCAAGGCACCTTCGAGGAGAAAAATTGGCCCTCTGAAAGAGAACGTCGAGCCACGTCAATG 761
Db 3541 AAGTCAAGGCACCTTCGAGGAGAAAAATTGGCCCTCTGAAAGAGAACGTCGAGCCACGTCAATG 3600
QY 762 ACCTTGCTCGCCAGCTTACCACCTTTGGGCACTTCCACCTATACCTTCAGCACTC 821
Db 3601 ACCTTGCTCGCCAGCTTACCACCTTTGGGCACTTCCACCTATACCTTCAGCACTC 3660
QY 822 TGAAGACCTGAACACACAGATGGAAGCTTCTGAGAGTGGCCGTCGAGGACCGAGTCAGGC 881
Db 3661 TGAAGACCTGAACACACAGATGGAAGCTTCTGAGAGTGGCCGTCGAGGACCGAGTCAGGC 3720
QY 882 AGCTGCATGAAGCCACAGGACTTTGGTCCAGATCTCAGCACTTTCTTCCAGCTGTG 941
Db 3721 AGCTGCATGAAGCCACAGGACTTTGGTCCAGATCTCAGCACTTTCTTCCAGCTGTG 3780
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1001

Db	3781	TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG	3840
QY	1002	AGACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAAGTCTTTAGCTG	1061
Db	3841	AGACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAAGTCTTTAGCTG	3900
QY	1062	ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA	1121
Db	3901	ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA	3960
QY	1122	AGGCCCTTTGCTTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCCTTGGACCAGCACA	1181
Db	3961	AGGCCCTTTGCTTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCCTTGGACCAGCACA	4020
QY	1182	ACCTCAAGCAAAATGACCAAGCCCATGGATATCCTGCGAGATTATTAATTGTTTGACCACTA	1241
Db	4021	ACCTCAAGCAAAATGACCAAGCCCATGGATATCCTGCGAGATTATTAATTGTTTGACCACTA	4080
QY	1242	TTTATGACCGCCTGGAGCAAGAGACAAACAATTTGGTCAACGTCCCTCTCTGCGGTGGATA	1301
Db	4081	TTTATGACCGCCTGGAGCAAGAGACAAACAATTTGGTCAACGTCCCTCTCTGCGGTGGATA	4140
QY	1302	TGTGCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC	1361
Db	4141	TGTGCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC	4200
QY	1362	TGCTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGAT	1421
Db	4201	TGCTCTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGAT	4260
QY	1422	ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTCC	1481
Db	4261	ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCAGGCTGGGCCTCC	4320
QY	1482	TTCTGTCATGATTTCTATCCAA	1501
Db	4321	TTCTGTCATGATTTCTATCCAA	4340

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RESULT 14
AAD37255
ID AAD37255 standard; DNA; 5149 BP.
XX
AC AAD37255;
XX
DT 21-AUG-2002 (first entry)
XX
DE Adeno-associated virus vector plasmid, AAV-MCK-delta4173.

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PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
XX Example 1; Page 57-59; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence

Sequence	5149 BP;	1489 A;	1236 C;	1269 G;	1155 T;	0 U;	0 Other;
Query Match	88.5%; Score 1328.8; DB 6; Length 5149;						
Best Local Similarity	99.5%; Pred. No. 0;						
Matches 1333; Conservative	0; Mismatches		7; Indels		0; Gaps		0;

XX
PT New dystrophin minigene for treating Duchenne or Becker muscular

QY 882 AGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCTG 941
Db |||||
QY 3810 AGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCTG 3869
Db |||||
QY 942 TCCAGGTCCTCTGGGAGAGAGCCCATCTCGCCAAACAAAGTCCCTACTATATCAACACG 1001
Db |||||
QY 3870 TCCAGGTCCTCTGGGAGAGAGCCCATCTCGCCAAACAAAGTCCCTACTATATCAACACG 3929
QY 1002 AGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGCTG 1061
Db |||||
QY 3930 AGACTCAAAACAACTTGTCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGCTG 3989
QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db |||||
QY 3990 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 4049
QY 1122 AGCCCTTTGCTGATCTCTTGAGCCTGTGAGTGCATGTGATGCCCTTGAGCCAGCAC 1181
Db |||||
QY 4050 AGCCCTTTGCTGATCTCTTGAGCCTGTGAGTGCATGTGATGCCCTTGAGCCAGCAC 4109
QY 1182 ACCTCAAGCAAAATGACAGCCCATGGATATCTGAGATTATTAATTGTTTGACCACTA 1241
Db |||||
QY 4110 ACCTCAAGCAAAATGACAGCCCATGGATATCTGAGATTATTAATTGTTTGACCACTA 4169
QY 1242 TTTATGACCGCTGGAGCAAGAGCACAACTTTGGTCAACGTCCTCTCTCGTGGATA 1301
Db |||||
QY 4170 TTTATGACCGCTGGAGCAAGAGCACAACTTTGGTCAACGTCCTCTCTCGTGGATA 4229
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC 1361
Db |||||
QY 4230 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC 4289
QY 1362 TGTCTTTAAACTGGCATCATTTCCCTGTGTAAGCACATTTTGAAGACAAAGTACAGAT 1421
Db |||||
QY 4290 TGTCTTTAAACTGGCATCATTTCCCTGTGTAAGCACATTTTGAAGACAAAGTACAGAT 4349
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCGCAGGCTGGGCCCTCC 1481
Db |||||
QY 4350 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCGCAGGCTGGGCCCTCC 4409
QY 1482 TTCTGCATGATTTCTATCCAA 1501
Db |||||
QY 4410 TTCTGCATGATTTCTATCCAA 4429

RESULT 15
ABK81998
ID ABK81998 standard; DNA; 5339 BP.
XX
AC ABK81998;
XX
DT 13-AUG-2002 (first entry)
XX
DE DNA encoding mini-dystrophin protein deltaR2-R21.
XX
KW Mini-dystrophin peptide; spectrin-like repeat domain; muscle disease;
KW Duchenne's muscular dystrophy; DMD; dystrophin; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200229056-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031126.
XX
PR 06-OCT-2000; 2000US-0238848P.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Chamberlain JS, Harper SQ;
XX

DR WPI; 2002-435334/46.
XX
PT A composition for preparing therapeutic drugs, has a mini-dystrophin
PT peptide comprising a specific number of spectrin-like repeat domains, or
PT a nucleic acid sequence encoding the mini-dystrophin peptide.
XX
PS Example 6; Fig 13; 145pp; English.
XX
CC The invention describes a composition comprising a mini-dystrophin
CC peptide comprising a spectrin-like repeat domain, where the domain
CC comprises n spectrin-like repeats, and contains no more than n spectrin-
CC like repeats, where n is an even number between 4-24, or a nucleic acid
CC encoding a mini-dystrophin peptide. The mini-dystrophin peptide or the
CC polynucleotide encoding it is useful as a medicament, for preparing a
CC drug for therapeutic application and in the preparation of a composition
CC for treatment of muscle disease, e.g. Duchenne's muscular dystrophy
CC (DMD). This sequence represents a mini-dystrophin sequence of the
CC invention
XX

SQ Sequence 5339 BP; 1638 A; 1191 C; 1187 G; 1323 T; 0 U; 0 Other;
Query Match 88.5%; Score 1328.8; DB 6; Length 5339;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTTCTGACCACTGGAAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db |||||
QY 1875 GGTCCCATTTGGAAGCCAGTTCTGACCACTGGAAGCGTCTGCACCTTTCTCTGCAGGAAC 1934
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGCG 281
Db |||||
QY 1935 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGCG 1994
QY 282 ACTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 341
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QY 1995 ACTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 2054
QY 342 CTAAAGAACCTGTAAATCATGAGTACTTCTTGAGACTGTACGATATTTCTGACAGAGCAGC 401
Db |||||
QY 2055 CTAAAGAACCTGTAAATCATGAGTACTTCTTGAGACTGTACGATATTTCTGACAGAGCAGC 2114
QY 402 CTTTGGAGGACTAGAGAACTCTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 461
Db |||||
QY 2115 CTTTGGAGGACTAGAGAACTCTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2174
QY 462 CCCAGAAATGTCACTCGGCTTCTACAAAGCAGGCTGAGGAGGTCATACTAGTGGGAAA 521
Db |||||
QY 2175 CCCAGAAATGTCACTCGGCTTCTACAAAGCAGGCTGAGGAGGTCATACTAGTGGGAAA 2234
QY 522 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGAGCTCC 581
Db |||||
QY 2235 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGAGCTCC 2294
QY 582 AGAACTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 641
Db |||||
QY 2295 AGAACTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2354
QY 642 AGGATCTCTGGCAGCCCGTGGGCGATCTCCTCATTTGAGTCTCTCCAAGATCACCTCGAGA 701
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QY 2355 AGGATCTCTGGCAGCCCGTGGGCGATCTCCTCATTTGAGTCTCTCCAAGATCACCTCGAGA 2414
QY 702 AAGTCAAGGCACTTCGAGGAGAAAAATTCGCGCTCTGAAAGAGAACTGAGCCACCTCAATG 761
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QY 2415 AAGTCAAGGCACTTCGAGGAGAAAAATTCGCGCTCTGAAAGAGAACTGAGCCACCTCAATG 2474
QY 762 ACCTTGTCTGCCAGCTTACCACTTTGGGCACTTACGCTCTCACCGTATACCTCAGCACTC 821
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QY 2475 ACCTTGTCTGCCAGCTTACCACTTTGGGCACTTACGCTCTCACCGTATACCTCAGCACTC 2534
QY 822 TGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCGCTCGAGGACCGAGTCAGGC 881
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QY 2535 TGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCGCTCGAGGACCGAGTCAGGC 2594

QY 882 AGTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCG 941
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2595 AGTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCG 2654
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1001
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Db |||||
3135 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAAGCGGCTGGGCCTCC 3194
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db |||||
3195 TTCTGCATGATTCTATCCAA 3214

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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 03:01:40 ; Search time 77.4052 Seconds
(without alignments)
10761.315 Million cell updates/sec

Title: US-09-845-416-12_COPY_1500_3000

Perfect score: 1501
Sequence: 1 agaagatctagaacaagaac.....ttctgcgatgattctatccaa 1501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 692709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1328.8	88.5	5952	4	US-09-687-875A-1 Sequence 1, Appli
2	1317.8	87.8	13977	4	US-09-484-970B-60 Sequence 60, Appl
C 3	1149.6	76.6	19307	3	US-08-836-022A-10 Sequence 10, Appl
C 4	1149.6	76.6	19307	3	US-09-427-048A-10 Sequence 10, Appl
5	547.4	36.5	6045	4	US-09-091-501B-7 Sequence 7, Appli
6	547.4	36.5	10320	4	US-09-091-501B-9 Sequence 9, Appli
7	517.8	34.5	3915	4	US-09-976-594-93 Sequence 93, Appl
8	69.8	4.7	200	4	US-09-091-501B-5 Sequence 5, Appli
9	69	4.6	200	4	US-09-091-501B-4 Sequence 4, Appli
10	65	4.3	200	4	US-09-091-501B-6 Sequence 6, Appli
C 11	53.4	3.6	7218	1	US-08-232-463-14 Sequence 14, Appl
12	44.2	2.9	2574	4	US-09-668-313A-10 Sequence 10, Appl
13	42.8	2.9	1690	4	US-09-620-312D-69 Sequence 69, Appl
14	42.8	2.9	7812	3	US-09-368-590-1 Sequence 1, Appli
15	38.6	2.6	1995	1	US-08-425-069-3 Sequence 3, Appli
16	38.6	2.6	1995	2	US-08-317-844B-3 Sequence 3, Appli
17	38.4	2.6	7672	4	US-09-220-132-24 Sequence 24, Appl
18	38.2	2.5	428	4	US-09-668-313A-3 Sequence 3, Appli
19	38.2	2.5	4439	4	US-09-668-313A-17 Sequence 17, Appl
C 20	34.8	2.3	1830121	4	US-09-557-884-1 Sequence 1, Appli
C 21	34.8	2.3	1830121	4	US-09-643-990A-1 Sequence 1, Appli
22	34.6	2.3	474	4	US-09-621-976-18033 Sequence 18033, A
C 23	34.6	2.3	2277	1	US-08-676-967-5 Sequence 5, Appli
C 24	34.6	2.3	2277	1	US-08-676-974-5 Sequence 5, Appli
C 25	34.6	2.3	2277	2	US-09-098-487-5 Sequence 5, Appli
26	34.4	2.3	1047	4	US-09-671-950-1 Sequence 1, Appli
27	34.4	2.3	1047	4	US-09-671-950-3 Sequence 3, Appli

28	34.4	2.3	1047	4	US-09-671-950-5 Sequence 5, Appli
29	34.4	2.3	1047	4	US-09-671-950-7 Sequence 7, Appli
30	34.4	2.3	1047	4	US-09-671-950-9 Sequence 9, Appli
31	34.4	2.3	1047	4	US-09-671-950-11 Sequence 11, Appl
32	34.4	2.3	1047	4	US-09-671-950-13 Sequence 13, Appl
33	34.2	2.3	750	4	US-08-961-527-370 Sequence 370, App
34	34.2	2.3	1620	4	US-08-858-207A-56 Sequence 56, Appl
35	34.2	2.3	2800	2	US-08-874-138-1 Sequence 1, Appli
36	34.2	2.3	2800	2	US-08-874-138-5 Sequence 5, Appli
37	34.2	2.3	2800	3	US-08-879-941-1 Sequence 1, Appli
38	34.2	2.3	2800	3	US-08-879-941-3 Sequence 3, Appli
39	34.2	2.3	2800	4	US-09-747-116-1 Sequence 1, Appli
40	34.2	2.3	2800	4	US-09-747-116-3 Sequence 3, Appli
41	34.2	2.3	32768	4	US-08-961-527-71 Sequence 71, Appl
42	34	2.3	648	4	US-09-252-991A-10033 Sequence 10033, A
C 43	34	2.3	762	4	US-09-252-991A-9821 Sequence 9821, Ap
44	34	2.3	1644	4	US-09-252-991A-10161 Sequence 10161, A
C 45	34	2.3	2235	3	US-09-153-804-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-687-875A-1
; Sequence 1, Application US/09687875A
; Patent No. 6544786
; GENERAL INFORMATION:
; APPLICANT: Xiao, Paul
; APPLICANT: Liu, Paul
; TITLE OF INVENTION: METHOD AND VECTOR FOR PRODUCING AND TRANSFERRING TRANS-SPLICED F
; FILE REFERENCE: 00792
; CURRENT APPLICATION NUMBER: US/09/687,875A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/158,868
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2897)..(2898)
; OTHER INFORMATION: S4 junction site
; NAME/KEY: misc feature
; LOCATION: (3198)..(3199)
; OTHER INFORMATION: S2 junction site
US-09-687-875A-1

Query Match	88.5%;	Score 1328.8;	DB 4;	Length 5952;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1333;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	162	GGGTTCTTTTACAAGACAGTTCTGACCACTGGAAGCGTCTGCACCTTCTCTGCAGGAAC	221	
Db	3284	GGTCCCATTTGGAAGCCAGTTCTGACCACTGGAAGCGTCTGCACCTTCTCTGCAGGAAC	3343	
QY	222	TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG	281	
Db	3344	TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG	3403	
QY	282	ACTTCCAGCAGTTTCAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA	341	
Db	3404	ACTTCCAGCAGTTTCAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA	3463	
QY	342	CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC	401	
Db	3464	CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC	3523	
QY	402	CTTTGGAAGGACTAGAGAAACTTACCAGAGCCCCAGAGAGCTGCCTCTCTGAGGAGAGAG	461	

Db 3524 CTTTGAAGGACTAGAGAACTCTACCAGGAGCCCGAGAGAGCTGCCTCCTGAGGAGAGAG 3583

Qy 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATATCTAGTGGGAAA 521

Db 3584 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATATCTAGTGGGAAA 3643

Qy 522 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 581

Db 3644 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 3703

Qy 582 AGGAACCTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCCAAGCTGAGGTGATCA 641

Db 3704 AGGAACCTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCCAAGCTGAGGTGATCA 3763

Qy 642 AGGATCCTGGCAGCCCCGTGGCGCATCTCTCATTGACTCTCTCCAAGATCAACCTCGAGA 701

Db 3764 AGGATCCTGGCAGCCCCGTGGCGCATCTCTCATTGACTCTCTCCAAGATCAACCTCGAGA 3823

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Db 3884 ACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCAGCTCTTCTTCCACGTCTG 3943

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Qy 882 AGCTGCATGAAGCCACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 941

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Qy 1422 ACCTTTTCAAGCAAGTGGAAGTTTCAACAGGATTTTGTGACCAAGCGAGGCTGGGCCCTCC 1481

Db 4544 ACCTTTTCAAGCAAGTGGAAGTTTCAACAGGATTTTGTGACCAAGCGAGGCTGGGCCCTCC 4603

Qy 1482 TTCTGCATGATTTCTATCCAA 1501

Db 4604 TTCTGCATGATTTCTATCCAA 4623

RESULT 2

US-09-484-970B-60
; Sequence 60, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 60
; LENGTH: 13977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 229357.11CB1
; NAME/KEY: unsure
; LOCATION: 11721-11761, 12294, 13969
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-60

Query Match 87.8%; Score 1317.8; DB 4; Length 13977;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 162 GGGTTCTTTTACAAGACAGTTCTGACCAGTGGAAAGCGTCTGCACCTTTTCTCTGCAGGAAC 221

Db 8598 GGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACCTTTTCTCTGCAGGAAC 8657

Qy 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGCG 281

Db 8658 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGCG 8717

Qy 282 ACTTTCCAGCAGTTTCAAGACGAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 341

Db 8718 ACTTTCCAGCAGTTTCAAGACGAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 8777

Qy 342 CTAAAGAACCTGTATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401

Db 8778 CTAAAGAACCTGTATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCAGC 8837

Qy 402 CTTTGAAGGACTAGAGAAACTCTACAGGAGCCCGAGAGAGCTGCCTCTCTGAGGAGAGAG 461

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Qy 522 AATTGAACCTGCATCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 581

Db 8958 AATTGAACCTGCATCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 9017

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Db 9018 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGTGAGGTGATCA 9077

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QY 1182 ACCTCAAGCAAAATGACCCATGGATATCCTGCAAGTATTAATTTGTTGACCACTA 1241
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QY 1481 CTTCTGCATGATTCTATCCAA 1501
Db 9918 CTTCTGCATGATTCTATCCAA 9938

RESULT 3

US-08-836-022A-10/c
; Sequence 10, Application US/08836022A
; Patent No. 6001557
; GENERAL INFORMATION:
; APPLICANT: Trustees of the University of Pennsylvania
; APPLICANT: Wilson, James M.
; APPLICANT: Fisher, Krishna J.
; APPLICANT: Chen, Shu-Jen
; APPLICANT: Weitzman, Matthew
; TITLE OF INVENTION: Improved Adenovirus Virus and
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,022A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,381
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GNVFN.008PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
US-08-836-022A-10

Query Match 76.6%; Score 1149.6; DB 3; Length 19307;
Best Local Similarity 91.1%; Pred.No. 0;
Matches 1221; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db 6096 GGTCCCAATTGGAAGCAAGTTCTGACCAGTGGAGCGTTTGATCTTTCTCTCAGGAAC 6037
QY 222 TTCTGCTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281
Db 6036 TTCTTGTGGCTACAGCTGAAAGATGATGAATTAAGCCCGTACGGCACCCATCGGTGGTG 5977
QY 282 ACTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 341
Db 5976 ATTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 5917
QY 342 CTAAGAACCTGTAAATCATGATGATCTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 5916 CTAAGAACCTGTAAATCATGATGATCTCTTGAGACTGTGAGAAATTTCTGACAGAGCAGC 5857
QY 402 CTTTGGAGGACTAGAGAACTCTACAGAGGAGCCAGAGAGTGCCTCTCTGAGGAGAGAG 461
Db 5856 CTTTGGAGGACTAGAGAACTCTACAGAGGAGCCAGAGAACTGCCTCTCTGAAGAAAGAG 5797
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 5796 CTCAGAAATGTCACTCGGCTCTACGAAAGCAGGCTGAAGAGGTCAACGCTGAATGGGACA 5737
QY 522 AATTGAACCTGCACCTCCGCTGACTGCGCAGAGAGAAATAGATGAGACCCCTTGAAAGACTCC 581
Db 5736 AATTGAACCTGCCTCAGCTGATTGGCAGAGAGAAATAGATGAAGCTCTTGAAAGACTCC 5677
QY 582 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 641
Db 5676 AGGAACCTTCAAGAGGCTGCCGATGAAGTGGACCTCAAGTTGGCCCAAGCTGAGGTGATCA 5617
QY 642 AGGATCCTTGGCAGCCCGTGGCGGATCTCTCATTTGACTCTCTCCAGATCACCTCGAGA 701
Db 5616 AGGATCCTTGGCAGCCAGTGGGGGATCTCTCATTTGACTCTCTGCAAGATCACCTTGAAA 5557
QY 702 AAGTCAAGGCACTTCGAGGAGAAATGGCGCTCTGAAAGAGAACTGAGGCCACGTCATG 761
Db 5556 AAGTCAAGGCACTTCGGGGAGAAATTCACCTCTTTAAAGAGAAATGTCATCGTCAATG 5497
QY 762 ACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 821
Db 5496 ACCTTGACATCAGCTGACCACACTGGGCATTCAGCTCTCACCTTATAACCTCAGCACTT 5437

QY 822 TGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 881
Db
QY 5436 TGAAGATCTGAATACACAGATGGAGGCTTCTACAGGTGGCTGTGGAGGACCGGTGCAGAC 5377
Db
QY 882 AGCTGATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCAGTCTG 941
Db
QY 5376 AGCTGCATGAAGCCCAACAGGACTTTGGTCTCTGCATCCAGCACTTCTCTTCCACTTCAG 5317
QY 942 TCCAGGTCCCTGGGAGAGAGCCATCTCGCCCAACAAAGTGCCTACTATATCAACCACG 1001
Db
QY 5316 TTCAGGTCCCTGGGAGAGAGCCATCTCACCAACAAAGTGCCTACTATATCAACCACG 5257
QY 1002 AGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 1061
Db
QY 5256 AGACCCAAACCACTTGTTGGGACCAACCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 5197
QY 1062 ACCTGAATAATGTGAGTTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db
QY 5196 ACCTGAATAATGTGAGTTCTCCGCTATAGGACTGCCATGAACTCAGAAGGCTCCAGA 5137
QY 1122 AGGCCCTTGCTTGATCTCTTGAGCTGTGAGCTGCATGTGATGCCCTTGAGCCAGCACA 1181
Db
QY 5136 AGGCCCTTGCTTGATCTCTTGAGCTGTGAGCTGCATGTGATGCCCTTGAGCCAGCACA 5077
QY 1182 ACCTCAAGCAAAATGACAGCCCAATGGATATCTCTGCAGATTATTAATTGTTTGACCACTA 1241
Db
QY 5076 ACCTCAAGCAAAATGACAGCCCAATGGATATCTCTGCAGATAATTAATGTTTGACTACAA 5017
QY 1242 TTTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAAGTCCCTCTCTGCGTGGATA 1301
Db
QY 5016 TTTATGATCGTCTGGAGCAAGAGCACAACAATCTGGTCAATGTCCCTCTCTGTGTGGATA 4957
QY 1302 TGTGTCTGAACCTGGCTGCTGATGTTTATGATACGGGACGAAACAGGAGGATCCCGTCTCC 1361
Db
QY 4956 TGTGTCTCAACTGGCTTCTCAATGTTTATGATACGGGACGAAACAGGAGGATCCCGTCTCC 4897
QY 1362 TGTCTTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACAATTTGGAAGACAAGTACAGAT 1421
Db
QY 4896 TGTCTTTTAAACCTGGCATCATTTCTGTGTAAAGCACAATTTGGAAGACAAGTACAGAT 4837
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACGCGCAGGCTGGGCCCTCC 1481
Db
QY 4836 ACCTTTTCAAGCAAGTGGCAAGTTTCAACTGGCTTTTGTGACCAAGCTAGGCTGGGTCTTC 4777
QY 1482 TTCTGCATGATCTATCCAA 1501
Db 4776 TTCTGCATGATCTATTCAA 4757

RESULT 5
US-09-091-501B-7
; Sequence 7, Application US/09091501B
; Patent No. 6518413
; GENERAL INFORMATION:
; APPLICANT: Tinsley, Jonathon M
; APPLICANT: Davies, Kay E
; TITLE OF INVENTION: Utrrophin gene expression
; FILE REFERENCE: 620-42
; CURRENT APPLICATION NUMBER: US/09/091,501B
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: PCT/GB96/03156
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: GB 9525962.8
; PRIOR FILING DATE: 1995-12-19
; PRIOR APPLICATION NUMBER: GB 9615797.9
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: GB 9622174.2
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6045

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(6037)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (724)..(758)
; OTHER INFORMATION: Precise residue is left open
US-09-091-501B-7

Query Match 36.5%; Score 547.4; DB 4; Length 6045;
Best Local Similarity 61.4%; Pred. No. 2.7e-167;
Matches 900; Conservative 0; Mismatches 556; Indels 9; Gaps 1;

QY 45 ACATGGTGGTGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTTGGGAAGAAC 104
Db 3270 ACAGGCAGAGATGGTAAAGCTTTGGGAAATTTCTGAAGAGGCTACTATGCTTCAACATC 3329
QY 105 AACTTAAGTATTTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAAACCGCTGGG 164
Db 3330 GACTGGATGATATGAACCAAGATGGAATGACTTAAAGCAAAATCTGCTAGCATCAGGG 3389
QY 165 TTCTTTTACAGACAGTTTCTGACCAGTGGGAAGCGTCTGCACCTTTTCTCTGCAGGAACCTC 224
Db 3390 CCCATTTGGAGCCAGCGCTGAGAAGTGAAGCAAGCTTAAAGAAACAAATGCCTATTGAGGAGATG 3449
QY 225 TGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGAGGCACCTATTGGAGCGGACT 284
Db 3450 TCAAATGGCTGAATATGAAGATGAAGAGCTTAAAGAAACAAATGCCTATTGAGGAGATG 3509
QY 285 TTCCAGCAGTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAACTA 344
Db 3510 TTCCAGCCTTACAGCTCCAGTATGACCATTTGAAGCCCTGAGACGGGAGTTAAAGGAGA 3569
QY 345 AAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTTGCACAGAGCAGCCTT 404
Db 3570 AAGAATATTTCTGCTCTGATGCTGTGACCCAGGCCCGAGTTTTTCTTGGCTGATCAGCCAA 3629
QY 405 T-----GGAAGGACTAGAGAACTCTACCAGGAGCCCGAGAGCTGCCTCTCTGAGG 455
Db 3630 TTGAGGCCCTTGAAGAGCCCAAGAAAGAACTTCAATCAAAAACAGAAATTAACCTCTGAGG 3689
QY 456 AGAGAGCCCAAGATGTCACTCGGCTTTACGAAAGCAGGCTGAGGAGGTCAATACTGAGT 515
Db 3690 AGAGAGCCCAAGATTTGCCAAAGCCATGCGCAAAACAGTCTTCTGAAGTCAAAGAAAAT 3749
QY 516 GGGAAAAATTGAACCTGCACCTCCGCTGACTGGGAGAAATTTGGCCTCTGAAAGAGAACCTGAGCCACG 575
Db 3750 GGGAAAGTCTAAATGCTGTAACCTAGCAATTTGGCAAAAGCAAGTGGACAAGGCATTGGAGA 3809
QY 576 GACTCCAGGAACCTTCAAGAGGCGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGG 635
Db 3810 AACTCAGAGACCTGCAGGGAGCTATGGATGACCTGGACGCTGACATGAAGGAGGCAGAGT 3869
QY 636 TGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCAC 695
Db 3870 CCGTGCAGGAATGCTGGAAGCCCGTGGGAGACTTACTCATTGACTCGCTGCAGGATCACA 3929
QY 696 TCGAGAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCCTCTGAAAGAGAACCTGAGCCACG 755
Db 3930 TTGAAAAAATCATGGCATTTAGAGAGAAATTTGCACCAATCAACTTAAAGTTAAACCG 3989
QY 756 TCAATGACCTTTGCTGCCAGCTTACCACCTTTGGGCATTTCAGCTCTCACCGTATAACCTCA 815
Db 3990 TGAATGATTTTCCAGTCAGCTGTCTCCACTTGACCTGTCATCCCTCTCTAAAGATGTCTC 4049
QY 816 GCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAG 875
Db 4050 GCCAGCTAGATGACCTTAATATGCGATGGAAACTTTTACAGGTTTTCTGTGGATGATCGCC 4109

QY 936 CGTCTGCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCA 995
Db |||||
8445 CGTCAGTCCAGTGCCTGGCAAGATCCATTTTCACATAATAAAGTGCCCTATTACATCA 8504
QY 996 ACCACGAGACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAAGTCTT 1055
Db |||||
8505 ACCATCAACACAGACCACCTGTTGGGACCATCCCAAAATGACCGAATCTTTCAATCCC 8564
QY 1056 TAGCTGACCTGAATAATGTACAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGAC 1115
Db |||||
8565 TTGCTGACCTGAATAATGTACGTTTTTCTGCCTACCGTACAGCAATCAAAATCCGAAGAC 8624
QY 1116 TGCAGAAGGCCCTTTGCTTGGAATCTTTGAGCCCTGTACAGTGCATGTGATGCTTGGACC 1175
Db |||||
8625 TACAANAAGCACTATGTTTGGATCTCTTAGAGTTGAGTACAAACAATGAATTTTCAAC 8684
QY 1176 AGCAAACTCAAGCAAAATGACCAGCCCATGGATATCCTGTCAGATTATTTAATTGTTGA 1235
Db |||||
8685 AGCAAACTTGAACCAAAATGACCAGCTCCTCAGTGTTCAGATGTCAATCACTGTCTGA 8744
QY 1236 CCACTATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCG 1295
Db |||||
8745 CAACAACCTTATGATGGACTTGAGCAAAATGCATAAGGACCTGGTCAACGTTCCACTCTGTG 8804
QY 1296 TGGATATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGCATCC 1355
Db |||||
8805 TTGATATGTGTCTCAATTTGGTTGCTCAATGTCTATGACAGGGGTGCAACTGGGAAAAATTA 8864
QY 1356 GTGTCCTGTCTTTTAAACTGGCATCATTTCCCTGTGTAAGACATTTTGGAAAGACAAGT 1415
Db |||||
8865 GAGTGCAGAGTCTGAAGATTGGATTAAATGTCTCTCTCCAAAGGTCTCTTTGGAGAAAAAT 8924
QY 1416 ACAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAGCGCAGGCTGG 1475
Db |||||
8925 ACAGATATCTCTTTAAGGAAGTTGCGGGGCCGACAGAAATGTGTGACCAGAGGCAGCTGG 8984
QY 1476 GCCTCCTTCTGTCATGATTCTATCCA 1500
Db |||||
8985 GCCTGTTACTTTCATGATGCCATCCA 9009

RESULT 7

US-09-976-594-93
; Sequence 93, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 93
; LENGTH: 3915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 290344.1
US-09-976-594-93

Query Match 34.5%; Score 517.8; DB 4; Length 3915;
Best Local Similarity 61.5%; Pred. No. 9e-158;
Matches 846; Conservative 0; Mismatches 527; Indels 2; Gaps 1;

QY 126 GATGGGCAACATCTGTAGATGGACAGAACCGCTGGGTTCTTTTACAGACAGATTTCTG 185
Db |||||

555 GTTGAATGAATAAAAAAAGTCTCAACACCTCCGCTCGCTAGAGGCCTTCTCAG 614

QY 186 ACCAGTGAAGCGTCTGCACTTTCTCTGCAGGAACCTTCTGGTGTGGCTACAGCTGAAAAG 245
Db |||||
615 ACCACAGTGGAAAGCTTCAGTCCCTCTTCAAGAGATTATTGACTGGCTCAGCCAAAAGG 674
QY 246 ATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTTCAGAAGCAGA 305
Db |||||
675 ATGAGGAGTTGTCAGTCTCAGTGGCCCTTACAGGGGATGTGGCCCTGGTGCAACAGGAGA 734
QY 306 ACGATGTACATAGGGCCTTCAAGAGGGAATTTGAAAACCTGTAATCATGAGTA 365
Db |||||
735 AGGAGACACATCGGCCCTTTATGGAAGAAAGTCAAGTCTCGGGGCCCTACATCTATTCTG 794
QY 366 CTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCCTTTGGAAGGACTAGAGAAACTCT 425
Db |||||
795 TGCTGGAGTCAGCTCAGGCCCTTCCCTGTCCAGCACCCATTTGAGGAGTTAGAGGAGCCTC 854
QY 426 ACCAGGAGCCCAAGAGAGCTGCCCTCCTGAGGAGAGAGCCCAAGAAATGTCACTCGGCTTCTAC 485
Db |||||
855 ATTCTGAGAGCAAAAGATACCTCCCGAAACAGCGGATCCAGAATCTCAGCCGCTTTGTAT 914
QY 486 GAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTTGAACCTGCACCTCGCTGACT 545
Db |||||
915 GGAAGCAGCGCAGCGTGGCCAGTGAATCTGGAGCAGCTCTTGGAGATTCAGGGG--CATGGAGG 974
QY 546 GGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCCAGGAATTTCAAGAGGCCACCGGATG 605
Db |||||
975 AGCACCGTCACTTGAAGCGGACTCTGGAGCAGCTCTTGGAGATTCAGGGG--CATGGAGG 1032
QY 606 AGCTGGACCTCAAGCTGCGCCAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCG 665
Db |||||
1033 AACTAAGCACTACTCTGAGCCAAAGCTGAGGGAGTCCGAGGCCACTTGGGAGCCCATTTGGGG 1092
QY 666 ATCTCCTCAATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAA 725
Db |||||
1093 ATCTCTTCAFTGATTCACTCCAGAGCACAATCCAGGCTATTAAAGCTGTTCAAAGAAGAAAT 1152
QY 726 TTGCGCCTCTGAAAAGAGAACGTGAGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTT 785
Db |||||
1153 TCTCCCCCATGAAAAGATGGAGTAAAGTTGGTGAATGATCTGGCCCAACCAACTTGCCATTT 1212
QY 786 TGGGCATTCAAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAAACACCAGATGGA 845
Db |||||
1213 CTGATGTGCACTTGTCAATGGAGAAATTCAGGCCCTTGGAAACAGATCAACGTCCGATGGA 1272
QY 846 AGCTTCTGCAGGTGGCCGTGAGGACCGAGTCAGGCAGCTGCAATGAAGCCCAAGGAGT 905
Db |||||
1273 AACAACTACAGCGTCAGTTGATGAGAGGCTTAAGCAGCTCCAGGATGCCACCGGAGT 1332
QY 906 TTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGCTCCCTGGGAGAGAGCCA 965
Db |||||
1333 TTGGCCTGGTTCACAGCACTTTCTCTCTCTCTGTCCAGGTTCCCTGGGAAAGAGCAA 1392
QY 966 TCTCGCCAAACAAAAGTGCCCTACTATATATCAACCAAGAGACTCAAAACAACTTGTGGGACC 1025
Db |||||
1393 TTTCAACCAATAAAGTTCCCTACTACATCAACCAAGGCTCAGACCAATGCTGGGACC 1452
QY 1026 ATCCCAAAATGACAGAGCTCTACCAAGTCTTTAGCTGACCTGAATAATGTGATTTCTCAG 1085
Db |||||
1453 ATCCCAAGATGACAGAGTTATACCAAAACCTTAGCTGATCTGAACAACATTAAAGTTCTCAG 1512
QY 1086 CTTATAGGACTGCCATGAAAACCTCCGAAGACTGCAGAAAGGCCCTTTGCTTGGATCTCTTGA 1145
Db |||||
1513 CTTATCGCACTGCCATGAAAACCTCCGAGAGTCCAGAAAGCCCTTGGCTTGGACCTGGTAA 1572
QY 1146 GCCTGTGAGTGTGATGCTTGGACCAGCACAACTCAAGCAAAATGACCAGCCCA 1205
Db |||||
1573 CTTTAAACCACAGCCCTGGAAATCTTCAATGAGCATGATCTGCAGGCCAGTGAGCACGTGA 1632
QY 1206 TGGATATCCTGCAGATTATTAATTTGTTGACCACCTATTTATGACCGCTGGAGCAAGAGC 1265
Db |||||
1633 TGGATGTGTAGAGGTCATTCACCTGCCTGACTGCCTTATATGAACGTTTGGAGGAGGAAA 1692
QY 1266 ACAACAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGTCTGAACTGGCTGTGAATG 1325


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; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 69
; LENGTH: 1690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(1522)
; US-09-620-312D-69

Query Match      2.9%; Score 42.8; DB 4; Length 1690;
Best Local Similarity 47.9%; Pred. No. 0.003;
Matches 156; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

QY 580 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCACAGCTGAGGTGAT 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 55 CAAGGAGTTGCACCAAGTTGGCGCACGACCTGGACACGAGCTGGCATGGGTTTCAGGAGCG 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 640 CAAGGGA---TCCTGGCAGCCCGTGGGGCGATCTCTCATTTGACTCTCTCCAGATCACCT 696
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 115 GCTGCCACTGGCCATGCACAGAGCGAGGCAACCGTTTGCAGGCGGTCCAGCAGCACAT 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 697 CGAGAAAGTCAAGGCACCTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACGTGAGCCACGT 756
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 CAAAAAGAACACAGGGCCTGCGCGGGAGATCCAGGCGCATGGCGCGCGCTGGAGGAGGT 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 757 CAATGACCTTGTCCGACCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAG 816
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 235 GCTGGAGCGCGCGCGCGCTGCGTGCCTGCGGAGCCCGGAGGCGAGGCGAGTGCGCCG 294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 817 CACTCTGGAAGACCTGAACACAGATGGAAGCTTCTGAGGTGGCGCTGAGGACCGAGT 876
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 295 GGGCCTGGAGCAGCTGCAGAGCGCTTGGCGCGACTGCGGAGGCTGCCGAGCGACGGCA 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 877 CAGGCAGCTGCATGAAGCCACAGGG 902
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 GCAGGTGCTGGACCGCGCGCTTCCAGG 380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-368-590-1
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; FILE REFERENCE: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
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; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
US-09-368-590-1

Query Match      2.9%; Score 42.8; DB 3; Length 7812;
Best Local Similarity 47.9%; Pred. No. 0.0083;
Matches 156; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

QY 580 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCACAGCTGAGGTGAT 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3639 CAAGGAGTTGCACCAAGTTGGCGCACGACCTGGACACGAGCTGGCATGGGTTTCAGGAGCG 3698
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 640 CAAGGGA---TCCTGGCAGCCCGTGGGGCGATCTCTCATTTGACTCTCTCCAGATCACCT 696
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3699 GCTGCCACTGGCCATGCACAGAGCGAGGCAACCGTTTGCAGGCGGTCCAGCAGCACAT 3758
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 697 CGAGAAAGTCAAGGCACCTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACGTGAGCCACGT 756
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3759 CAAAAAGAACACAGGGCCTGCGCGGGAGATCCAGGCGCATGGCGCGCGCTGGAGGAGGT 3818
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 757 CAATGACCTTGTCCGACCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAG 816
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3819 GCTGGAGCGCGCGCGCTGCGTGCCTGCGGAGCCCGGAGGCGAGGCGAGTGCGCCG 3878
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 817 CACTCTGGAAGACCTGAACACAGATGGAAGCTTCTGAGGTGGCGCTGAGGACCGAGT 876
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3879 GGGCCTGGAGCAGCTGCAGAGCGCTTGGCGCGACTGCGGAGGCTGCCGAGCGACGGCA 3938
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 877 CAGGCAGCTGCATGAAGCCACAGGG 902
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3939 GCAGGTGCTGGACCGCGCGCTTCCAGG 3964
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RESULT 15
US-08-425-069-3
; Sequence 3, Application US/08425069
; Patent No. 5728810
; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V.
; APPLICANT: Xu, Ming
; APPLICANT: Hinman, Michael B.
; TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
; TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
; TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 No. 5728810th Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,069
; FILING DATE: 19-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1447-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1995 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: p6B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1785
; US-08-425-069-3

Query Match      2.6%; Score 38.6; DB 1; Length 1995;
Best Local Similarity 44.0%; Pred. No. 0.078;
Matches 164; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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QY      410 GGACTAGAGAAACTCTACAGGAGCCCGAGAGCTGCGCCTCTGAGGAGAGAGCCCGCAGAAT 469
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QY      470 GTCACCTGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAAC 529
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QY      530 CTGCACTCCGCTGACTGGCAGAGAAAAAATAGATGAGACCCCTTGAAAGACTCCAGGAACTT 589
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Db      1031 CAGGAGGATATGGACCCAGGTAGTGCATCTGCAGCAGCAGCAGCCGACGACCTGGACAAAC 1090

QY      650 TGGCAGCCCGTGG 662
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Db      1091 AAGGACCGAGGAGG 1103
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Search completed: September 19, 2004, 11:06:59
Job time : 81.4052 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 08:30:27 ; Search time 500.133 Seconds
(without alignments)
15148.395 Million cell updates/sec

Title: US-09-845-416-12_COPY_1500_3000

Perfect score: 1501

Sequence: 1 agaagatctagaacaagaac.....ttctgcatgattctatccaa 1501

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1501	100.0	3510	10	US-09-845-416-12 Sequence 12, Appl
2	1501	100.0	4476	10	US-09-845-416-31 Sequence 31, Appl
3	1328.8	88.5	2169	10	US-09-845-416-4 Sequence 4, Appl
4	1328.8	88.5	3531	10	US-09-845-416-10 Sequence 10, Appl
5	1328.8	88.5	3858	10	US-09-845-416-9 Sequence 9, Appl
6	1328.8	88.5	3999	10	US-09-845-416-6 Sequence 6, Appl
7	1328.8	88.5	4182	10	US-09-845-416-2 Sequence 2, Appl
8	1328.8	88.5	4498	10	US-09-845-416-30 Sequence 30, Appl
9	1328.8	88.5	4825	10	US-09-845-416-29 Sequence 29, Appl
10	1328.8	88.5	4848	10	US-09-845-416-35 Sequence 35, Appl
11	1328.8	88.5	4966	10	US-09-845-416-28 Sequence 28, Appl
12	1328.8	88.5	4990	10	US-09-845-416-34 Sequence 34, Appl
13	1328.8	88.5	5060	10	US-09-845-416-36 Sequence 36, Appl
14	1328.8	88.5	5149	10	US-09-845-416-27 Sequence 27, Appl

15	1328.8	88.5	5339	16	US-10-149-736-40	Sequence 40, Appl
16	1328.8	88.5	5462	16	US-10-149-736-41	Sequence 41, Appl
17	1328.8	88.5	8689	16	US-10-149-736-42	Sequence 42, Appl
18	1328.8	88.5	11058	10	US-09-845-416-1	Sequence 1, Appl
19	1328.8	88.5	11443	16	US-10-149-736-44	Sequence 44, Appl
20	1328.8	88.5	12057	16	US-10-149-736-47	Sequence 47, Appl
21	1328.8	88.5	13957	9	US-09-782-378A-22	Sequence 22, Appl
22	1328.8	88.5	13957	9	US-09-880-107-2284	Sequence 2284, Ap
23	1328.8	88.5	13957	16	US-10-149-736-1	Sequence 1, Appl
24	1328.8	88.5	14069	13	US-10-342-887-434	Sequence 434, App
25	1328.8	88.5	14069	13	US-10-172-118-434	Sequence 434, App
26	1328.8	88.5	14082	13	US-10-342-887-981	Sequence 981, App
27	1328.8	88.5	14082	13	US-10-172-118-981	Sequence 981, App
28	1328.8	88.5	14082	16	US-10-341-434-108	Sequence 108, App
29	1324	88.2	1821	10	US-09-845-416-13	Sequence 13, Appl
30	1149.6	76.6	13815	16	US-10-149-736-2	Sequence 2, Appl
31	1041	69.4	3446	10	US-09-845-416-14	Sequence 14, Appl
32	1041	69.4	4414	10	US-09-845-416-32	Sequence 32, Appl
33	1011.6	67.4	5417	16	US-10-149-736-39	Sequence 39, Appl
34	937	62.4	1434	10	US-09-845-416-15	Sequence 15, Appl
35	555.6	37.0	10705	12	US-10-152-319A-1598	Sequence 1598, Ap
36	554.2	36.9	11096	16	US-10-149-736-4	Sequence 4, Appl
37	547.4	36.5	10302	9	US-09-782-378A-23	Sequence 23, Appl
38	547.4	36.5	10302	16	US-10-149-736-3	Sequence 3, Appl
39	538.6	35.9	16531	15	US-10-101-510-667	Sequence 667, App
40	527.4	35.1	5106	13	US-10-220-120-157	Sequence 157, App
41	393	26.2	887	16	US-10-149-736-35	Sequence 35, Appl
42	387	25.8	387	16	US-10-149-736-32	Sequence 32, Appl
43	324	21.6	324	16	US-10-149-736-33	Sequence 33, Appl
44	216	14.4	216	16	US-10-149-736-34	Sequence 34, Appl
45	185.4	12.4	1991	10	US-09-845-416-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-845-416-12
; Sequence 12, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 3510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-12

Query Match	100.0%;	Score 1501;	DB 10;	Length 3510;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1501;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY	1	AGAAGATCTAGAACAAAGAACAGTCAGGGTCAATTCTCTCACTACATGGTGGTGTAGT	60	
Db	1500	AGAAGATCTAGAACAAAGAACAGTCAGGGTCAATTCTCTCACTACATGGTGGTGTAGT	1559	
QY	61	TGATGAATCTAGTGGAGATCAGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG	120	
Db	1560	TGATGAATCTAGTGGAGATCAGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG	1619	
QY	121	AGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCGCTGGGTCTTTTACAAGACAG	180	
Db	1620	AGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCGCTGGGTCTTTTACAAGACAG	1679	

QY 181 TTCTGACCAGTGAAGCGTCTGCACCTTTCTCTGCAGGAACCTTCTGGTGTGGCTACAGCT 240
Db 1680 TTCTGACCAGTGAAGCGTCTGCACCTTTCTCTGCAGGAACCTTCTGGTGTGGCTACAGCT 1739
QY 241 GAAAGATGATGAATTAAGCCGCGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTTCAGAA 300
Db 1740 GAAAGATGATGAATTAAGCCGCGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTTCAGAA 1739
QY 301 GCAGAACGATGTACATAGGCGCTTCAAGAGGGGAATTGAAAACTAAAGAACCTGTAATCAT 360
Db 1800 GCAGAACGATGTACATAGGCGCTTCAAGAGGGGAATTGAAAACTAAAGAACCTGTAATCAT 1859
QY 361 GAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCCTTTGGAGGACTAGAGAA 420
Db 1860 GAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCCTTTGGAGGACTAGAGAA 1919
QY 421 ACTCTACAGAGGCCAGAGAGCTGCCTCTCTGAGGAGAGGCCAGAAATGTCACTCGGCT 480
Db 1920 ACTCTACAGAGGCCAGAGAGCTGCCTCTCTGAGGAGAGGCCAGAAATGTCACTCGGCT 1979
QY 481 TCTACGAAAGCAGGCTGAGAGGTTCAATACTGAGTGGGAAAAATTTGAACCTGCACCTCCGC 540
Db 1980 TCTACGAAAGCAGGCTGAGAGGTTCAATACTGAGTGGGAAAAATTTGAACCTGCACCTCCGC 2039
QY 541 TGACTGGCAGAGAAAAATAGATGAGACCCCTTTGAAAGACTCCAGGAACCTTCAAGAGGCCAC 600
Db 2040 TGACTGGCAGAGAAAAATAGATGAGACCCCTTTGAAAGACTCCAGGAACCTTCAAGAGGCCAC 2039
QY 601 GGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGTGATCAAGGGATCCTGGCAGCCCGT 660
Db 2100 GGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGTGATCAAGGGATCCTGGCAGCCCGT 2159
QY 661 GSGCGATCTCCTCATTTGACTCTCTCCAAGATCAGCTCGAGAAAGTCAAGGCACCTTCGAGG 720
Db 2160 GSGCGATCTCCTCATTTGACTCTCTCCAAGATCAGCTCGAGAAAGTCAAGGCACCTTCGAGG 2219
QY 721 AGAAATTCGCGCTCTGAAAGAGAACGCTGAGCCACGTCATGACCTTGTCTGCCAGCTTAC 780
Db 2220 AGAAATTCGCGCTCTGAAAGAGAACGCTGAGCCACGTCATGACCTTGTCTGCCAGCTTAC 2279
QY 781 CACTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAG 840
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QY 901 GGAATTTGGTCCAGCATCTCAGCACTTTCTTTCCAGCTCTGTCCAGGGTCCCTGGGAGAG 960
Db 2400 GGAATTTGGTCCAGCATCTCAGCACTTTCTTTCCAGCTCTGTCCAGGGTCCCTGGGAGAG 2459
QY 961 AGCCATCTCGCCAAACAAGTGCCCTACTATATCAACACAGAGACTCAAAACAACCTTGCTG 1020
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QY 1201 GCCCATGGATATCCTGCGAGATTATTAATTGTTGACCACCTATTATGACCGCCTGGAGCA 1260
Db 2700 GCCCATGGATATCCTGCGAGATTATTAATTGTTGACCACCTATTATGACCGCCTGGAGCA 2759
QY 1261 AGAGCAACAATAATTTGGTCAACGTCCTCTCTGCGCTGGATATGTGTGACACTGGCTGCT 1320

Db 2760 AGAGCAACAATAATTTGGTCAACGTCCTCTCTGCGCTGGATATGTGTCTGAACCTGGCTGCT 2819
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Db 2820 GAATGTTTATGATACGGGACGAACAGGAGGATCGGTGTCTCTCTTTTAAAACTGGCAT 2879
QY 1381 CATTTCCCTGTGTAAGCACATTTTGAAGACAAAGTACAGATACCTTTTCAAGCAAGTGGC 1440
Db 2880 CATTTCCCTGTGTAAGCACATTTTGAAGACAAAGTACAGATACCTTTTCAAGCAAGTGGC 2939
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QY 1501 A 1501
Db 3000 A 3000

RESULT 2
US-09-845-416-31
; Sequence 31, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 4476
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-31

Query Match 100.0%; Score 1501; DB 10; Length 4476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGCAACAACTTAAGGTATTGGG 120
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QY 121 AGATCGATGGGCAACATCTGTAGATGGACAGAACGCGCTGGGTTCTTTTACAAGACAG 180
Db 2376 AGATCGATGGGCAACATCTGTAGATGGACAGAACGCGCTGGGTTCTTTTACAAGACAG 2435
QY 181 TTCTGACCAGTGGAGCGCTCTGCACCTTTCTCTGAGGAACCTTCTGGTGTGGCTACAGCT 240
Db 2436 TTCTGACCAGTGGAGCGCTCTGCACCTTTCTCTGAGGAACCTTCTGGTGTGGCTACAGCT 2495
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QY 361 GAGTACTCTTGAGACTGTACGAATATTTTCTGACAGAGCAGCCCTTTGGAAGGACTAGAGAA 420
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QY 421 ACTCTACCAGGAGCCAGAGAGCTGCCTCCTGAGGAGAGAGCCAGAAATGTCACTCGGCT 480
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QY GGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAAGGGATCCTGSCAGCCCGT 660
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2856 GGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAAGGGATCCTGSCAGCCCGT 2915
QY GGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCCACTTCGAGG 720
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Db |||||
3036 CACTTTGGGCATTACAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAG 3095
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Db |||||
3096 ATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAAGCAGCTGCATGAAGCCACAG 3155
QY GGACTTTGGTCCAGCATCTCAGCACTTCTTCCACGTCTGTCCAGGTCCTCGGAGAG 960
Db |||||
3156 GGACTTTGGTCCAGCATCTCAGCACTTCTTCCACGTCTGTCCAGGTCCTCGGAGAG 3215
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3456 GCCCATGGATATCCTGCGAGATTATTAATTGTTTGACCCACTATTTATGACCCGCTGGAGCA 3515
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QY CATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGC 1440
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3696 AAGTTC AACAGGATTTTGTGACCCAGCGAGGCTGGGCCCTCCTTCTGTCATGATTCTATCCA 3755
QY 1501 A 1501

Db 3756 A 3756

RESULT 3

US-09-845-416-4
; Sequence 4, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-4

Query Match 88.5%; Score 1328.8; DB 10; Length 2169;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAGTGGGAAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db |||||
333 GGTCCCAATTGGAAGCCAGTTCTGACCAGTGGGAAGCGTCTGCACCTTTCTCTGCAGGAAC 392
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281
Db |||||
393 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 452
QY 282 ACTTTCCAGCAGTTTCAAGCAGAACGATGTACATAGGSCCTTCAAGAGGGAATTGAAAA 341
Db |||||
453 ACTTTCCAGCAGTTTCAAGCAGAACGATGTACATAGGSCCTTCAAGAGGGAATTGAAAA 512
QY 342 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db |||||
513 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 572
QY 402 CTTTGGAGGACTAGAGAAAACCTCTACCAGGAGCCCAGAGAGCTGCCTCCTTGAGGAGAG 461
Db |||||
573 CTTTGGAGGACTAGAGAAAACCTCTACCAGGAGCCCAGAGAGCTGCCTCCTTGAGGAGAG 632
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db |||||
633 CCCAGAAATGTCACTCGGCTTCTACGAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 692
QY 522 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 581
Db |||||
693 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 752
QY 582 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 641
Db |||||
753 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 812
QY 642 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGA 701
Db |||||
813 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGA 872
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCTCTGAAAGAGAACGTGAGCCACGTCAATG 761
Db |||||
873 AAGTCAAGGCACCTTCGAGGAGAAATTGCGCTCTGAAAGAGAACGTGAGCCACGTCAATG 932
QY 762 ACCTTGCTCGCCAGCTTACCACCTTTGGSCATTGAGCTCTCACCGTATAACCTCAGCACTC 821
Db |||||
933 ACCTTGCTCGCCAGCTTACCACCTTTGGSCATTGAGCTCTCACCGTATAACCTCAGCACTC 992

QY	1242	TTTATGACCGCCTGGAGCAAGAGACAAACAATTGGTCAACGTCCCTCTCTGCGTGATA	1301
DB	2762	TTTATGACCGCCTGGAGCAAGAGACAAACAATTGGTCAACGTCCCTCTCTGCGTGATA	2821
QY	1302	TGTGCTGAACCTGGTGCTGAATGTTTATGATACGGACGAACAGGGAGGATCCGTGTCC	1361
DB	2822	TGTGCTGAACCTGGTGCTGAATGTTTATGATACGGACGAACAGGGAGGATCCGTGTCC	2881
QY	1362	TGTCTTTTAAACTGSCATCATTTCCCTGTGTTAAAGCACATTTGGAAGACAAGTACAGAT	1421
DB	2882	TGTCTTTTAAACTGSCATCATTTCCCTGTGTTAAAGCACATTTGGAAGACAAGTACAGAT	2941
QY	1422	ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGGCTCC	1481
DB	2942	ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGGCTCC	3001
QY	1482	TTCTGCATGATTCATCCAA	1501
DB	3002	TTCTGCATGATTCATCCAA	3021

RESULT 5

US-09-845-416-9

; Sequence 9, Application US/09845416

; Publication No. US20030171312A1

; GENERAL INFORMATION:

; APPLICANT: XIAO, XIAO

; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: DE1142

; CURRENT APPLICATION NUMBER: US/09/845,416

; CURRENT FILING DATE: 2001-04-30

; PRIOR APPLICATION NUMBER: 60/200,777

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 3858

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-845-416-9

RESULT 6

US-09-845-416-6

; Sequence 6, Application US/09845416

Publication No. US20030171312A1

GENERAL INFORMATION:

APPLICANT: XIAO, XIAO

100; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-6

Query Match 88.5%; Score 1328.8; DB 10; Length 3999;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTCTTACCAAGTGGAGCGTCTGCACCTTTCTCTGCAGGAAC 221
DB |||||
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGGCG 281
DB |||||
QY 2210 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGGCG 2269
DB |||||
QY 282 ACTTTCAGCAGTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 341
DB |||||
QY 2270 ACTTTCAGCAGTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 2329
DB |||||
QY 342 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
DB |||||
QY 2330 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 2389
DB |||||
QY 402 CTTTGAAGGACTAGAGAAACTCTACCAGGAGCCAGAGAGCTGCCCTCGTGGAGGAGAG 461
DB |||||
QY 2390 CTTTGAAGGACTAGAGAAACTCTACCAGGAGCCAGAGAGCTGCCCTCGTGGAGGAGAG 2449
DB |||||
QY 462 CCCAGAAATGTCACTCGGCTTTACGAAAGCAGGTGAGGAGGTCAATACTAGTGGGAAA 521
DB |||||
QY 2450 CCCAGAAATGTCACTCGGCTTTACGAAAGCAGGTGAGGAGGTCAATACTAGTGGGAAA 2509
DB |||||
QY 522 AATTGAACCTGCACCTCCGTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 581
DB |||||
QY 2510 AATTGAACCTGCACCTCCGTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 2569
DB |||||
QY 582 AGGAACCTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCCAAGCTGAGGTGATCA 641
DB |||||
QY 2570 AGGAACCTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCCAAGCTGAGGTGATCA 2629
DB |||||
QY 642 AGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGA 701
DB |||||
QY 2630 AGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGA 2689
DB |||||
QY 702 AAGTCAAGGCACTTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACCGTGAGCCACGTCAATG 761
DB |||||
QY 2690 AAGTCAAGGCACTTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACCGTGAGCCACGTCAATG 2749
DB |||||
QY 762 ACCTTGCTCGCCAGCTTACCACCTTTGGGCAATCAGCTCTCACCGTATAACCTCAGCACTC 821
DB |||||
QY 2750 ACCTTGCTCGCCAGCTTACCACCTTTGGGCAATCAGCTCTCACCGTATAACCTCAGCACTC 2809
DB |||||
QY 822 TGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTTGGCCGTCGAGGACCGAGTCAGGC 881
DB |||||
QY 2810 TGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTTGGCCGTCGAGGACCGAGTCAGGC 2869
DB |||||
QY 882 ASCTGCATGAAGCCCAAGGAGTCTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 941
DB |||||
QY 2870 ASCTGCATGAAGCCCAAGGAGTCTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 2929
DB |||||
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1001
DB |||||
QY 2930 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 2989
DB |||||

QY 1002 AGACTCAAAACAACCTTGTGGGACCATCCCAAATGACAGAGCTCTACAGTCTTTAGCTG 1061
DB |||||
QY 2990 AGACTCAAAACAACCTTGTGGGACCATCCCAAATGACAGAGCTCTACAGTCTTTAGCTG 3049
DB |||||
QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGA 1121
DB |||||
QY 3050 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGA 3109
DB |||||
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGTCATGTGATGCCCTTGGACGACACA 1181
DB |||||
QY 3110 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGTCATGTGATGCCCTTGGACGACACA 3169
DB |||||
QY 1182 ACCTCAAGCAAAATGACAGCCCATGGATATCTCTGACAGATTATTAATTGTTGACCACTA 1241
DB |||||
QY 3170 ACCTCAAGCAAAATGACAGCCCATGGATATCTCTGACAGATTATTAATTGTTGACCACTA 3229
DB |||||
QY 1242 TTTATGACCGCTGGAGCAAGAGCACAACAATTGGTCAACGTCCTCTCTCGCTGGATA 1301
DB |||||
QY 3230 TTTATGACCGCTGGAGCAAGAGCACAACAATTGGTCAACGTCCTCTCTCGCTGGATA 3289
DB |||||
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 1361
DB |||||
QY 3290 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 3349
DB |||||
QY 1362 TGTCTTTTAAACTGCGCATCATTTCCCTGTGTAAAGCACATTTTGGAGACAAGTACAGAT 1421
DB |||||
QY 3350 TGTCTTTTAAACTGCGCATCATTTCCCTGTGTAAAGCACATTTTGGAGACAAGTACAGAT 3409
DB |||||
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAGCGCAGCTGGCCCTCC 1481
DB |||||
QY 3410 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAGCGCAGCTGGCCCTCC 3469
DB |||||
QY 1482 TTCTGCATGATTCTATCCAA 1501
DB |||||
QY 3470 TTCTGCATGATTCTATCCAA 3489
DB |||||

RESULT 7

US-09-845-416-2
; Sequence 2, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-2

Query Match 88.5%; Score 1328.8; DB 10; Length 4182;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTCTTACCAAGTGGAGCGTCTGCACCTTTCTCTGCAGGAAC 221
DB |||||
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGGCG 281
DB |||||
QY 2393 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGGCG 2452
DB |||||
QY 282 ACTTTCAGCAGTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 341
DB |||||

Db 2453 ACTTTCAGCAGTTTCAGAACAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 2512
QY 342 CTAAAGAACCTGTAATCATCAGTACTCTTGAGACTGTACGAATATTTCTGCAGAGCAGC 401
Db 2513 CTAAAGAACCTGTAATCATCAGTACTCTTGAGACTGTACGAATATTTCTGCAGAGCAGC 2572
QY 402 CTTTGAAGGACTAGAGAACTCTACCAGGAGCCACAGAGAGCTGCCCTCCTGAGGAGAG 461
Db 2573 CTTTGAAGGACTAGAGAACTCTACCAGGAGCCACAGAGAGCTGCCCTCCTGAGGAGAG 2632
QY 462 CCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 2633 CCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 2692
QY 522 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 581
Db 2693 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 2752
QY 582 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCAAAGCTGAGGTGATCA 641
Db 2753 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCAAAGCTGAGGTGATCA 2812
QY 642 AGGATCCTGGCAGCCCGTGGCGCATCTCCTCATTTGACTCTCTCCAAGATCACTCGAGA 701
Db 2813 AGGATCCTGGCAGCCCGTGGCGCATCTCCTCATTTGACTCTCTCCAAGATCACTCGAGA 2872
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGCTGAGCCACGTC AATG 761
Db 2873 AAGTCAAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAGAGAACGCTGAGCCACGTC AATG 2932
QY 762 ACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 821
Db 2933 ACCTTGCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 2992
QY 822 TGGAAACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCGTCGAGGACCGAGTCAGGC 881
Db 2993 TGGAAACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCGTCGAGGACCGAGTCAGGC 3052
QY 882 AGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCAGCTCTG 941
Db 3053 AGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCAGCTCTG 3112
QY 942 TCCAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACCACG 1001
Db 3113 TCCAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTTACTATATCAACCACG 3172
QY 1002 AGACTCAAAACAACTTGCTGGGACCATCTGCCAAACAAAGTGCCTTACTATATCAACCACG 1061
Db 3173 AGACTCAAAACAACTTGCTGGGACCATCTGCCAAACAAAGTGCCTTACTATATCAACCACG 3232
QY 1062 ACCTGAATAATGTGAGTTCTCAGTTATAGGACTGCCATGAAACTCCGAAGACTGCAG 1121
Db 3233 ACCTGAATAATGTGAGTTCTCAGTTATAGGACTGCCATGAAACTCCGAAGACTGCAG 3292
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCCTTGGACCAAGCA 1181
Db 3293 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCCTTGGACCAAGCA 3352
QY 1182 ACCTCAAGCAAAATGACCAAGCCATGGATATCCTGCAGATTATTAATTGTTGACCACTA 1241
Db 3353 ACCTCAAGCAAAATGACCAAGCCATGGATATCCTGCAGATTATTAATTGTTGACCACTA 3412
QY 1242 TTTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCTCTCTCGTGGATA 1301
Db 3413 TTTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCTCTCTCGTGGATA 3472
QY 1302 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGCTGCC 1361
Db 3473 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGCTGCC 3532
QY 1362 TGTCTTTTAAACTGGCATCATTTTCCCTGTGTAAGCACATTTGGAAGACAAGTACAGAT 1421
Db 3533 TGTCTTTTAAACTGGCATCATTTTCCCTGTGTAAGCACATTTGGAAGACAAGTACAGAT 3592

QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTACCAGCGCAGGCTGGGCTCC 1481
Db 3593 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTACCAGCGCAGGCTGGGCTCC 3652
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 3653 TTCTGCATGATTCTATCCAA 3672

RESULT 8

US-09-845-416-30
; Sequence 30, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-30

Query Match 88.5%; Score 1328.8; DB 10; Length 4498;
Best Local Similarity 99.5%; Pred.No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db 2439 GGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGAAC 2498
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281
Db 2499 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 2558
QY 282 ACTTTCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAA 341
Db 2559 ACTTTCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAA 2618
QY 342 CTAAAGAACCTGTAATCATGAGTACTTCTGAGACTGTACGAATATTTCTGCAGAGCAGC 401
Db 2619 CTAAAGAACCTGTAATCATGAGTACTTCTGAGACTGTACGAATATTTCTGCAGAGCAGC 2678
QY 402 CTTTGAAGGACTAGAGAACTCTACAGGAGCCCAGAGAGTGCCTCCTGAGGAGAG 461
Db 2679 CTTTGAAGGACTAGAGAACTCTACAGGAGCCCAGAGAGTGCCTCCTGAGGAGAG 2738
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAA 521
Db 2739 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAA 2798
QY 522 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 581
Db 2799 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 2858
QY 582 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTCGGCAAGCTGAGGTGATCA 641
Db 2859 AGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTCGGCAAGCTGAGGTGATCA 2918
QY 642 AGGATCCTGGCAGCCCGTGGCGCATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGA 701
Db 2919 AGGATCCTGGCAGCCCGTGGCGCATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGA 2978
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTTGGCCTCTGAAAGAGAACGTCGAGCCACGTC AATG 761

Db 2979 AAGTCAGGCACCTTCGAGGAGAAATTGGCCCTCTGAAAGAGAAACGTGAGCCACGTCATG 3038
QY 762 ACCTTGCTGCCAGCTTACCACCTTTGGGCATTTCAGCTCTCACCGTATACCTCAGCACTC 821
Db 3039 ACCTTGCTGCCAGCTTACCACCTTTGGGCATTTCAGCTCTCACCGTATACCTCAGCACTC 3098
QY 822 TGGAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 881
Db 3099 TGGAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 3158
QY 882 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 941
Db 3159 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 3218
QY 942 TCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1001
Db 3219 TCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 3278
QY 1002 AGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGCTG 1061
Db 3279 AGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGCTG 3338
QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3339 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3398
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGTGCATGTGATGCCCTGGACCAACA 1181
Db 3399 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGTGCATGTGATGCCCTGGACCAACA 3458
QY 1182 ACCTCAAGCAAAATGACAGGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTA 1241
Db 3459 ACCTCAAGCAAAATGACAGGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTA 3518
QY 1242 TTTATGACCGCCTGGAGCAAGAGCACAAACATTTGGTCAACGTCCTCTCTCGGTGGATA 1301
Db 3519 TTTATGACCGCCTGGAGCAAGAGCACAAACATTTGGTCAACGTCCTCTCTCGGTGGATA 3578
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 1361
Db 3579 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 3638
QY 1362 TGTCTTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTGGAGACAAAGTACAGAT 1421
Db 3639 TGTCTTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTGGAGACAAAGTACAGAT 3698
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCCAGCGAGGCTGGCCCTCC 1481
Db 3699 ACCITTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCCAGCGAGGCTGGCCCTCC 3758
QY 1482 TTCTGCATGATTTCTATCCAA 1501
Db 3759 TTCTGCATGATTTCTATCCAA 3778

RESULT 9
US-09-845-416-29
; Sequence 29, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4825
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-845-416-29
Query Match 88.5%; Score 1328.8; DB 10; Length 4825;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 162 GGGTTCTTTTACAAGACAGATTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db 2766 GGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGAAC 2825
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCCACCTATTGGAGCG 281
Db 2826 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCCACCTATTGGAGCG 2885
QY 282 ACTTTCCAGCAGTTTCAGAACGAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 341
Db 2886 ACTTTCCAGCAGTTTCAGAACGAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 2945
QY 342 CTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 2946 CTAAAGAACCTGTATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 3005
QY 402 CTTTGGAGGACTAGAGAAACTCTACAGAGGCCAGAGAGCTGCCCTCTGAGGAGAGAG 461
Db 3006 CTTTGGAGGACTAGAGAAACTCTACAGAGGCCAGAGAGCTGCCCTCTGAGGAGAGAG 3065
QY 462 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATFACTAGTGGGAAA 521
Db 3066 CCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATFACTAGTGGGAAA 3125
QY 522 AATTGAACCTGCATCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTTGAAAGACTCC 581
Db 3126 AATTGAACCTGCATCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTTGAAAGACTCC 3185
QY 582 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTCGCCAAAGCTGAGGTGATCA 641
Db 3186 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTCGCCAAAGCTGAGGTGATCA 3245
QY 642 AGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGA 701
Db 3246 AGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGA 3305
QY 702 AAGTCAAGGCACCTTCGAGGAGAAAAATTCGCGCTCTGAAAGAGAACGTGAGCCACGTCATG 761
Db 3306 AAGTCAAGGCACCTTCGAGGAGAAAAATTCGCGCTCTGAAAGAGAACGTGAGCCACGTCATG 3365
QY 762 ACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATACCTCAGCACTC 821
Db 3366 ACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATACCTCAGCACTC 3425
QY 822 TGGAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 881
Db 3426 TGGAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 3485
QY 882 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGCTCTG 941
Db 3486 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGCTCTG 3545
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCACG 1001
Db 3546 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCACG 3605
QY 1002 AGACTCAAAACAACTTGTCTGGGACCATCCCAAAAATGACAGAGCTCTACCACTCTTTAGCTG 1061
Db 3606 AGACTCAAAACAACTTGTCTGGGACCATCCCAAAAATGACAGAGCTCTACCACTCTTTAGCTG 3665
QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3666 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3725
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGTGCATGTGATGCCCTGGACCAACA 1181

Db 3726 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCCTTGACCAGCACA 3785
QY 1182 ACTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAAATTGTTGACCACTA 1241
Db 3786 ACTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAAATTGTTGACCACTA 3845
QY 1242 TTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGATA 1301
Db 3846 TTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGATA 3905
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC 1361
Db 3906 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC 3965
QY 1362 TGTCTTTTAAACTGGCATCATCTCCCTGTGTAAAGCACATTTGGAAGACAACTACAGAT 1421
Db 3966 TGTCTTTTAAACTGGCATCATCTCCCTGTGTAAAGCACATTTGGAAGACAACTACAGAT 4025
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCC 1481
Db 4026 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCC 4085
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 4086 TTCTGCATGATTCTATCCAA 4105

RESULT 10
US-09-845-416-35
; Sequence 35, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DB1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 35
; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-35

Query Match 88.5%; Score 1328.8; DB 10; Length 4848;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 162 GGGTTCTTTTACAAGACAGTTCTGACGAGTGGAAGCGTCTGCACCTTTCTCTGCAGAAC 221
Db 2789 GGTCCCATTTGGAAGCCAGTTCTGACCAGTGAAGCGTCTGCACCTTTCTCTGCAGAAC 2848
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGAGGCACCTATTGGAGGCG 281
Db 2849 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGAGGCACCTATTGGAGGCG 2908
QY 282 ACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 341
Db 2909 ACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 2968
QY 342 CTAAAGAACCTGTAATCATGAGTACTTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 2969 CTAAAGAACCTGTAATCATGAGTACTTTGAGACTGTACGAATATTTCTGACAGAGCAGC 3028
QY 402 CTTTGGAGGACTAGAGAACTCTACAGGAGCCCGAGAGCTGCCCTCTCTGAGGAGAGAG 461
Db 3029 CTTTGGAGGACTAGAGAACTCTACAGGAGCCCGAGAGCTGCCCTCTCTGAGGAGAGAG 3088
QY 462 CCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521

Db 3089 CCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGGCTGAGAGGTCAATACTAGTGGGAAA 3148
QY 522 AATTGAACCTGCACCTCCGCTCACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 581
Db 3149 AATTGAACCTGCACCTCCGCTCACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 3208
QY 582 AGGAACTTCAAGAGGCGCACGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 641
Db 3209 AGGAACTTCAAGAGGCGCACGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 3268
QY 642 AGGATCCTGGCAGCCCGTGGGCGATCTCCTCAATTGACTCTCTCCAAGATCACCTCGAGA 701
Db 3269 AGGATCCTGGCAGCCCGTGGGCGATCTCCTCAATTGACTCTCTCCAAGATCACCTCGAGA 3328
QY 702 AAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCATG 761
Db 3329 AAGTCAAGGCACCTTCGAGGAGAAATTTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCATG 3388
QY 762 ACCTTGTCTGCCAGCTTACCACCTTTGGGCGATTCAGCTCTCACCGTATAACCTCAGCACTC 821
Db 3389 ACCTTGTCTGCCAGCTTACCACCTTTGGGCGATTCAGCTCTCACCGTATAACCTCAGCACTC 3448
QY 822 TGGAAAGACCTGAACACCAAGATGGAAGCTTCTGCAGGTGGCGCTCGAGGACCGAGTCAGGC 881
Db 3449 TGGAAAGACCTGAACACCAAGATGGAAGCTTCTGCAGGTGGCGCTCGAGGACCGAGTCAGGC 3508
QY 882 AGCTGCATGAAGCCCAACAGGAGCTTTGGTCCAGCATCTCAGCACTTCTTCCACGCTCTG 941
Db 3509 AGCTGCATGAAGCCCAACAGGAGCTTTGGTCCAGCATCTCAGCACTTCTTCCACGCTCTG 3568
QY 942 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1001
Db 3569 TCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 3628
QY 1002 AGACTCAAAACAACTTGTCTGGGACCAATCCCAAATAATGACAGAGCTTACCAGTCTTTAGCTG 1061
Db 3629 AGACTCAAAACAACTTGTCTGGGACCAATCCCAAATAATGACAGAGCTTACCAGTCTTTAGCTG 3688
QY 1062 ACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3689 ACCTGAATAATGTGAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3748
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCTGATGATGCTTTGGACCACTA 1181
Db 3749 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCTGATGATGCTTTGGACCACTA 3808
QY 1182 ACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAAATTGTTGACCACTA 1241
Db 3809 ACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAAATTGTTGACCACTA 3868
QY 1242 TTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGATA 1301
Db 3869 TTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCTCTCTGCGTGGATA 3928
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC 1361
Db 3929 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCC 3988
QY 1362 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAACTACAGAT 1421
Db 3989 TGTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAACTACAGAT 4048
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCC 1481
Db 4049 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCC 4108
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 4109 TTCTGCATGATTCTATCCAA 4128

RESULT 11

QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGGCG 281
Db 2991 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACCTATTGGAGGCG 3050
QY 282 ACTTTCCAGCAGTTTCAAGACAGAAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAAA 341
Db 3051 ACTTTCCAGCAGTTTCAAGACAGAAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAAA 3110
QY 342 CTAAAGAAACCTGTATATCATAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 3111 CTAAAGAAACCTGTATATCATAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 3170
QY 402 CTTTGGAGGACTAGAGAAACTCTACCAGGAGCCACAGAGAGCTGCCTCCTGAGGAGAGAG 461
Db 3171 CTTTGGAGGACTAGAGAAACTCTACCAGGAGCCACAGAGAGCTGCCTCCTGAGGAGAGAG 3230
QY 462 CCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 3231 CCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 3290
QY 522 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 581
Db 3291 AATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAATAGATGAGACCCCTTGAAGACTCC 3350
QY 582 AGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 641
Db 3351 AGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 3410
QY 642 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 701
Db 3411 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGA 3470
QY 702 AAGTCAAGGCACCTTCAGAGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATG 761
Db 3471 AAGTCAAGGCACCTTCAGAGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATG 3530
QY 762 ACCTTGCTCGCCAGCTTACCACTTTGGGCATTACGCTCTCACCGTATAACCTCAGCACTC 821
Db 3531 ACCTTGCTCGCCAGCTTACCACTTTGGGCATTACGCTCTCACCGTATAACCTCAGCACTC 3590
QY 822 TGAAGACCTGAACACCAAGATGGAAGCTTCTGCAGTGGCCGTCGAGGACCGAGTCAGGC 881
Db 3591 TGAAGACCTGAACACCAAGATGGAAGCTTCTGCAGTGGCCGTCGAGGACCGAGTCAGGC 3650
QY 882 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCTG 941
Db 3651 AGCTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCTG 3710
QY 942 TCCAGGTCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCACG 1001
Db 3711 TCCAGGTCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCACG 3770
QY 1002 AGACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 1061
Db 3771 AGACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 3830
QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3831 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3890
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCCTTGGACCCAGACA 1181
Db 3891 AGGCCCTTTGCTTGGATCTCTTGAGCCCTGTGAGCTGCATGTGATGCCTTGGACCCAGACA 3950
QY 1182 ACCTCAAGCAAAATGACCAAGCCATGGATATCCTGAGATTATTAATTGTTTGACCACTA 1241
Db 3951 ACCTCAAGCAAAATGACCAAGCCATGGATATCCTGAGATTATTAATTGTTTGACCACTA 4010
QY 1242 TTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 1301
Db 4011 TTTATGACCGCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 4070
QY 1302 TGTGCTGAAGTGGCTGCTGAATGTTTATGATACGGGACGAAAGGAGGATCCCGTGTC 1361

Db 4071 TGTGCTGAAGTGGCTGCTGAATGTTTATGATACGGACGAAACAGGAGGATCCGTGTCC 4130
QY 1362 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAAGTACAGAT 1421
Db 4131 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTTGAAGACAAAGTACAGAT 4190
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGGCTCC 1481
Db 4191 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGGCTGGGCTCC 4250
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 4251 TTCTGCATGATTCTATCCAA 4270

RESULT 13
US-09-845-416-36
; Sequence 36, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 5060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-36

Query Match 88.5%; Score 1328.8; DB 10; Length 5060;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 162 GGGTTCTTTTACAAGACAGTTCTGACCAAGTGGAAAGCGTGTGACACCTTTCTCTGCAGGAAC 221
Db 3001 GGTCCCATTTGGAAGCCAGTTCTGACCAAGTGGAAAGCGTGTGACACCTTTCTCTGCAGGAAC 3060
QY 222 TTCTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281
Db 3061 TTCTGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 3120
QY 282 ACTTTCCAGCAGTTTCAAGACAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 341
Db 3121 ACTTTCCAGCAGTTTCAAGACAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAA 3180
QY 342 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 401
Db 3181 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGC 3240
QY 402 CTTTGGAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAG 461
Db 3241 CTTTGGAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAG 3300
QY 462 CCCAGAAATGTCACCTGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 3301 CCCAGAAATGTCACCTGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 3360
QY 522 AATTGAACCTTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 581
Db 3361 AATTGAACCTTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCC 3420
QY 582 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 641
Db 3421 AGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCA 3480

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QY 642 AGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAAGATCACCTCGAGA 701
Db 3481 AGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAAGATCACCTCGAGA 3540
QY 702 AAGTCAAGGCACCTTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACTGAGCCACGTCAATG 761
Db 3541 AAGTCAAGGCACCTTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACTGAGCCACGTCAATG 3600
QY 762 ACCTTGCTGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCGTATTAACCTCAGCACTC 821
Db 3601 ACCTTGCTGCCAGCTTACCACTTTGGGCAATTCAGCTCTCACCGTATTAACCTCAGCACTC 3660
QY 822 TGAAGACCTGAACACACAGATGGAAGCTTCTGCAAGTGGCCGTGAGGACCGAGTCAGGC 881
Db 3661 TGAAGACCTGAACACACAGATGGAAGCTTCTGCAAGTGGCCGTGAGGACCGAGTCAGGC 3720
QY 882 AGCTGCATGAAGCCCAAGGACCTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 941
Db 3721 AGCTGCATGAAGCCCAAGGACCTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 3780
QY 942 TCCAGGCTCCCTGGGAGAGAGCCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1001
Db 3781 TCCAGGCTCCCTGGGAGAGAGCCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 3840
QY 1002 AGACTCAAAACAACCTTGCTGGGACCATCCCAAATGACAGAGCTCTACAGTCTTTAGCTG 1061
Db 3841 AGACTCAAAACAACCTTGCTGGGACCATCCCAAATGACAGAGCTCTACAGTCTTTAGCTG 3900
QY 1062 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1121
Db 3901 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 3960
QY 1122 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGTCATGTGATGCTTGGACCAACA 1181
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QY 1182 ACCTCAAGCAAAATGACCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 1241
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QY 1242 TTTATGACCGCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 1301
Db 4081 TTTATGACCGCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 4140
QY 1302 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGTCC 1361
Db 4141 TGTGCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGTCC 4200
QY 1362 TGTCTTTTAAACCTGGCATCATTTCCCTCTGTAAAGCACATTTTGAAGACAAAGTACAGAT 1421
Db 4201 TGTCTTTTAAACCTGGCATCATTTCCCTCTGTAAAGCACATTTTGAAGACAAAGTACAGAT 4260
QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCCAGGCTGGGCCCTCC 1481
Db 4261 ACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCCAGGCTGGGCCCTCC 4320
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db 4321 TTCTGCATGATTCTATCCAA 4340
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RESULT 14
US-09-845-416-27
; Sequence 27, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777

; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 5149
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-27

Query Match 88.5%; Score 1328.8; DB 10; Length 5149;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 162 GGGTCTTTTACAAGACAGTTCTGACCAAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGAAC 221
Db 3090 GGTCCCATTTGGAAGCCAGTTCTGACCAAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGAAC 3149
QY 222 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 281
Db 3150 TTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCG 3209
QY 282 ACTTTCAGCAGTTTCAAGACGAAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 341
Db 3210 ACTTTCAGCAGTTTCAAGACGAAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 3269
QY 342 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTTGACAGAGCAGC 401
Db 3270 CTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTTGACAGAGCAGC 3329
QY 402 CTTTGAAGGACTAGAGAAACTCTACCAAGAGCCCGAGAGAGCTGCTCTCTGAGGAGAGAG 461
Db 3330 CTTTGAAGGACTAGAGAAACTCTACCAAGAGCCCGAGAGAGCTGCTCTCTGAGGAGAGAG 3389
QY 462 CCCAGAAATGCTACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 521
Db 3390 CCCAGAAATGCTACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAA 3449
QY 522 AATTGAACCTGCACCTCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 581
Db 3450 AATTGAACCTGCACCTCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAAGACTCC 3509
QY 582 AGGAACTTCAAGAGGCCACGGATGAGTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 641
Db 3510 AGGAACTTCAAGAGGCCACGGATGAGTGGACCTCAAGCTGCGCAAGCTGAGGTGATCA 3569
QY 642 AGGATCCTGGCAGCCCGTGGCGGATCTCTCATTGACTCTCTCAAGATCACCTCGAGA 701
Db 3570 AGGATCCTGGCAGCCCGTGGCGGATCTCTCATTGACTCTCTCAAGATCACCTCGAGA 3629
QY 702 AAGTCAAGGCACCTTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACTGAGCCACGTCAATG 761
Db 3630 AAGTCAAGGCACCTTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACTGAGCCACGTCAATG 3689
QY 762 ACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 821
Db 3690 ACCTTGCTCGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTC 3749
QY 822 TGAAGACCTGAAACACACAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAGGC 881
Db 3750 TGAAGACCTGAAACACACAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAGGC 3809
QY 882 AGCTGCATGAAGCCCAAGGACCTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 941
Db 3810 AGCTGCATGAAGCCCAAGGACCTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTG 3869
QY 942 TCCAGGTCCTCTGGGAGAGAGCCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1001
Db 3870 TCCAGGTCCTCTGGGAGAGAGCCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 3929
QY 1002 AGACTCAAAACAACCTTGCTGGGACCATCCCAAATGACAGAGCTCTACAGTCTTTAGCTG 1061
Db 3930 AGACTCAAAACAACCTTGCTGGGACCATCCCAAATGACAGAGCTCTACAGTCTTTAGCTG 3989
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QY 1422 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGAGGCTGGGCCCTCC 1481
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3135 ACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGAGGCTGGGCCCTCC 3194
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1482 TTCTGCATGATTCTATCCAA 1501
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3195 TTCTGCATGATTCTATCCAA 3214
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: September 19, 2004, 15:14:18
Job time : 503.133 secs

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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 07:39:06 ; Search time 543.946 Seconds
(without alignments)
15627.746 Million cell updates/sec

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Perfect score: 2001
Sequence: 1 ggcagttcattgatggagag.....cattgagccaagtgtccgga 2001

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
5:	Geneseqn2001bs:*
6:	Geneseqn2002s:*
7:	Geneseqn2003as:*
8:	Geneseqn2003bs:*
9:	Geneseqn2003cs:*
10:	Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2001	100.0	3446	6	AAD37242	Aad37242 Human dys
2	1990	99.5	4414	6	AAD37260	Aad37260 Adeno-ass
3	1820.8	91.0	5417	6	ABK81997	Abk81997 DNA encod
4	1593	79.6	3510	6	AAD37240	Aad37240 Human dys
5	1593	79.6	4476	6	AAD37259	Aad37259 Adeno-ass
6	1332	66.6	4402	3	AZ48568	Aaz48568 A rod sho
7	1269.2	63.4	4402	3	AZ48567	Aaz48567 A rod sho
8	1263	63.1	3858	6	AAD37237	Aad37237 Human dys
9	1263	63.1	4825	6	AAD37257	Aad37257 Adeno-ass
10	1263	63.1	4848	6	AAD37263	Aad37263 Adeno-ass
11	1263	63.1	5060	6	AAD37264	Aad37264 Adeno-ass
12	1254	62.7	5339	6	ABK81998	Abk81998 DNA encod
13	1251.2	62.5	3531	6	AAD37238	Aad37238 Human dys
14	1251.2	62.5	4498	6	AAD37258	Aad37258 Adeno-ass
15	1245	62.2	4182	6	AAD37230	Aad37230 Human dys
16	1245	62.2	5149	6	AAD37255	Aad37255 Adeno-ass
17	1132.2	56.6	5462	6	ABK81999	Abk81999 DNA encod
18	1112	55.6	3999	6	AAD37234	Aad37234 Human dys
19	1112	55.6	4966	6	AAD37256	Aad37256 Adeno-ass
20	1112	55.6	4990	6	AAD37262	Aad37262 Adeno-ass
21	1002.6	50.1	1821	6	AAD37241	Aad37241 Human dys
22	1002.6	50.1	2169	6	AAD37232	Aad37232 Human dys
23	1002.6	50.1	5952	5	AAD06794	Aad06794 Human dys

24	1002.6	50.1	8689	6	ABK82000	Abk82000 DNA encod
25	1002.6	50.1	11058	6	AAD37229	Aad37229 Human dys
26	1002.6	50.1	11241	6	ABK82005	Abk82005 CDNA enco
27	1002.6	50.1	11443	6	ABK82002	Abk82002 DNA encod
28	1002.6	50.1	12923	1	AAN90338	Aan90338 Sequence
29	1002.6	50.1	13957	6	ABK81959	Abk81959 CDNA enco
30	1002.6	50.1	13957	6	ABT10904	Abt10904 Human bre
31	1002.6	50.1	13957	6	ABN95786	Abn95786 Gene #228
32	1002.6	50.1	13957	6	ABS69900	Abs69900 Human dys
33	1001	50.0	1434	6	AAD37243	Aad37243 Human dys
34	991.6	49.6	13977	6	ABS70403	Abs70403 Human bon
35	985.8	49.3	1991	6	AAD37231	Aad37231 Human dys
36	869.8	43.5	13815	6	ABK81960	Abk81960 CDNA enco
37	869.8	43.5	13815	6	ABI99799	Abi99799 Mouse isc
38	869.8	43.5	19307	2	AAT27558	Aat27558 Shuttle v
39	868.2	43.4	13815	2	AAV18885	Aav18885 Mus muscu
40	767	38.3	3275	1	AAN97129	Aan97129 Partial s
41	735.4	36.8	4075	3	AZ48569	Aaz48569 A rod sho
42	731.2	36.5	3747	3	AZ48566	Aaz48566 A rod sho
43	677.6	33.9	3163	3	AZ48571	Aaz48571 A rod sho
44	665	33.2	1667	6	AAD37235	Aad37235 Human dys
45	567.4	28.4	2005	7	ABT33376	Abt33376 NOVX DNA

ALIGNMENTS

RESULT 1
AAD37242
ID AAD37242 standard; DNA; 3446 BP.
XX
AC AAD37242;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human dystrophin minigene delta3447.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene.

Example 1; Page 53-54; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular

CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta3447 containing nucleotides 1-1992 (N-terminus,
CC hinge H1 and rods R1, R2 and R3), 8749-10227 (rod R24, hinge H4 and CR
CC domain) and 11047-11058 (dystrophin last 3 amino acids)
XX
SQ Sequence 3446 BP; 1074 A; 766 C; 787 G; 819 T; 0 U; 0 Other;

Query Match 100.0%; Score 2001; DB 6; Length 3446;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACACAGCTTTAGAAGAA 60
DB 1000 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACACAGCTTTAGAAGAA 1059

QY 61 GTATTATCGTGGCTTTCTGCTGAGGACACATTCGAAAGCACAAGGAGAGATTTCTAAT 120
DB 1060 GTATTATCGTGGCTTTCTGCTGAGGACACATTCGAAAGCACAAGGAGAGATTTCTAAT 1119

QY 121 GATGTGGAAGTGGTGAAGAACCAAGTTTCATATCATGAGGGGTACATGATGATTTGACA 180
DB 1120 GATGTGGAAGTGGTGAAGAACCAAGTTTCATATCATGAGGGGTACATGATGATTTGACA 1179

QY 181 GCCCATCAGGGCCGGTGGTAAATATTCATACTCATGAGGGGTACATGATGATTTGACA 240
DB 1180 GCCCATCAGGGCCGGTGGTAAATATTCATACTCATGAGGGGTACATGATGATTTGACA 1239

QY 241 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGATCTCTAAATTCAGA 300
DB 1240 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGATCTCTAAATTCAGA 1299

QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAGAAACAAAGCAATTTACATAGAGTTTAAATG 360
DB 1300 TGGGAATGCCTCAGGGTAGCTAGCATGGAAGAAACAAAGCAATTTACATAGAGTTTAAATG 1359

QY 361 GATCTCCAGAAATCGAAACTGAAGAGTTGAATGACTGGCTAACAAAACAGAAGAAAGAA 420
DB 1360 GATCTCCAGAAATCGAAACTGAAGAGTTGAATGACTGGCTAACAAAACAGAAGAAAGAA 1419

QY 421 CAAGGAAATGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTTAAACGCCAAGTAC 480
DB 1420 CAAGGAAATGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTTAAACGCCAAGTAC 1479

QY 481 AACAAACATAAGTGCTTCAAGAAGATCTAGAACAAAGAACAGTCAAGGTCAATTTCTCTCA 540
DB 1480 AACAAACATAAGTGCTTCAAGAAGATCTAGAACAAAGAACAGTCAAGGTCAATTTCTCTCA 1539

QY 541 CTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGAACTGCTGCTTTGGAAG 600
DB 1540 CTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGAACTGCTGCTTTGGAAG 1599

QY 601 AACAACTTAAGGTATTGGGAGATCGATGGGCAACATCTGTAGATGGACAGAAGACCGCT 660
DB 1600 AACAACTTAAGGTATTGGGAGATCGATGGGCAACATCTGTAGATGGACAGAAGACCGCT 1659

QY 661 GGGTCTTTTACAAGACATCCTTCTCAAAATGGCAACGCTTCTACTGAAGAACAGTGGCTTT 720
DB 1660 GGGTCTTTTACAAGACATCCTTCTCAAAATGGCAACGCTTCTACTGAAGAACAGTGGCTTT 1719

QY 721 TTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAAGATTCACACAACTGGCTTTA 780
DB 1720 TTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAAGATTCACACAACTGGCTTTA 1779

QY 781 AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCGTTTTAAAAGCGGATCTAG 840
DB 1780 AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCGTTTTAAAAGCGGATCTAG 1839

QY 841 AAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAAGATCTTTTCAACAC 900
DB 1840 AAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAAGATCTTTTCAACAC 1899

QY 901 TGAAGATAAGTCAGTGACCCAGAACGGAAGCATGGCTGGATAACTTTGCCCGGTGTT 960
DB

DB 1900 TGAAGAATAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGTT 1959
QY 961 GGGATAATTTAGTCCAAAAAACTTTGAAAAGAGTACAGCACAGACCCCTTGAAGACTCCAGG 1020
DB 1960 GGGATAATTTAGTCCAAAAAACTTTGAAAAGAGTACAGCACAGACCCCTTGAAGACTCCAGG 2019
QY 1021 AACTTCAAGAGGCCCGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAGG 1080
DB 2020 AACTTCAAGAGGCCCGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAGG 2079
QY 1081 GATCCTGGCAGCCCGTGGGGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGAAAG 1140
DB 2080 GATCCTGGCAGCCCGTGGGGGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGAAAG 2139
QY 1141 TCAAGGCACCTTCGAGGAGAAATTTGGCCCTCTGAAAAGAGAACGTAAGCCAGTCAATGACC 1200
DB 2140 TCAAGGCACCTTCGAGGAGAAATTTGGCCCTCTGAAAAGAGAACGTAAGCCAGTCAATGACC 2199
QY 1201 TTGCTCGCCAGCTTACCACTTTTGGGCAATTCAGCTCTCAACCGTATAACCTCAGCACTCTGG 1260
DB 2200 TTGCTCGCCAGCTTACCACTTTTGGGCAATTCAGCTCTCAACCGTATAACCTCAGCACTCTGG 2259
QY 1261 AAGACCTGAACACAGATGGAAGCTTTTGGTCCAGCATCTCAGCACTTTTCCACGTCCTGCTCC 1380
DB 2320 TGCATGAAGCCCAAGGGACTTTTGGTCCAGCATCTCAGCACTTTTCCACGTCCTGCTCC 2379
QY 1381 AGGTCCTCGGAGAGAGCCATCTCGCAAAACAAAGTGCCTACTATATCAACCCAGAGA 1440
DB 2380 AGGTCCTCGGAGAGAGCCATCTCGCAAAACAAAGTGCCTACTATATCAACCCAGAGA 2439
QY 1441 CTCAAAACAACTTGTGGGACCATCTCGCAAAACAAAGTGCCTACTATATCAACCCAGAGA 1500
DB 2440 CTCAAAACAACTTGTGGGACCATCTCGCAAAACAAAGTGCCTACTATATCAACCCAGAGA 2499
QY 1501 TGAATAATGTCAGATTTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGAAAG 1560
DB 2500 TGAATAATGTCAGATTTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGAAAG 2559
QY 1561 CCCTTTGCTTGGATCTCTTGAGCCCTGTTCAGCTGCATGTGATGCTTGGACCAGCACACC 1620
DB 2560 CCCTTTGCTTGGATCTCTTGAGCCCTGTTCAGCTGCATGTGATGCTTGGACCAGCACACC 2619
QY 1621 TCAAGCAAAATGACACAGCCCATGGATATCTCTGCAGATTTATTAATTTGTTGACCACTATTT 1680
DB 2620 TCAAGCAAAATGACACAGCCCATGGATATCTCTGCAGATTTATTAATTTGTTGACCACTATTT 2679
QY 1681 ATGACCCGCTGGAGCAAGAGCAACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGT 1740
DB 2680 ATGACCCGCTGGAGCAAGAGCAACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGT 2739
QY 1741 GTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACGAGAGGAGATCCGTCCTCTCT 1800
DB 2740 GTCTGAAGTGGCTGCTGAATGTTTATGATACGGGACGAGAGGAGATCCGTCCTCTCT 2799
QY 1801 CTTTAAACACTGGCATCATTTCCCTGTGTAAAGCAATTTGGAAGCAAGTACAGATACC 1860
DB 2800 CTTTAAACACTGGCATCATTTCCCTGTGTAAAGCAATTTGGAAGCAAGTACAGATACC 2859
QY 1861 TTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACAGCGCAGGCTGGCCTCTCTC 1920
DB 2860 TTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACAGCGCAGGCTGGCCTCTCTC 2919
QY 1921 TGCATGATTTCTATCCAAATTCGAAGACAGTTGGTGAAGTTGCATCCTTTGGGGGACAGTA 1980
DB 2920 TGCATGATTTCTATCCAAATTCGAAGACAGTTGGTGAAGTTGCATCCTTTGGGGGACAGTA 2979
QY 1981 ACATTGAGCCCAAGTGTCCGGA 2001
DB 2980 ACATTGAGCCCAAGTGTCCGGA 3000

||||| 1937 GCCCATCAGGCCGGTGGTAATATTTCTACAATTGGGAAGTAAGCTGATGGAACAGGA 1996
QY 241 AAATTATCAGAAGATCAAGAAACTGAAGTACAAGAGCAGATGAATCTCTAAATTCAAGA 300
Db 1997 AAATTATCAGAAGATCAAGAAACTGAAGTACAAGAGCAGATGAATCTCTAAATTCAAGA 2056
QY 301 TGGGAATGCCTCAGGTAGCTAGCATGGAAACAAAGCAATTTACATAGAGTTTAAATG 360
Db 2057 TGGGAATGCCTCAGGTAGCTAGCATGGAAACAAAGCAATTTACATAGAGTTTAAATG 2116
QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGA 419
Db 2117 GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGA 2176
QY 420 ACAAGGAAAAATGGAGGAAGAGCCTCTTTGGACCTGATCTTGAAGACCTTAAACGCCAAAGTA 479
Db 2177 ACAAGGAAAAATGGAGGAAGAGCCTCTTTGGACCTGATCTTGAAGACCTTAAACGCCAAAGTA 2236
QY 480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAAACAAAGCAAGTCAGGGTCAATTTCTCTC 539
Db 2237 CAACAACATAAGGTGCTTCAAGAAGATCTAGAAACAAAGCAAGTCAGGGTCAATTTCTCTC 2296
QY 540 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
Db 2297 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 2356
QY 600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCCG 659
Db 2357 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCCG 2416
QY 660 TGGGTTCTTTTACAAGACATCCTTTCTCAAATGGCAACGCTTTACTGAAGAACAGTGCCTT 719
Db 2417 TGGGTTCTTTTACAAGACATCCTTTCTCAAATGGCAACGCTTTACTGAAGAACAGTGCCTT 2476
QY 720 TTTAGTGCATGGCTTTTACAAAAAGAAAGATGCAGTGAACAAGATTCACACAACTGGCTTT 779
Db 2477 TTTAGTGCATGGCTTTTACAAAAAGAAAGATGCAGTGAACAAGATTCACACAACTGGCTTT 2536
QY 780 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTTTTTAAAGCGGATCTA 839
Db 2537 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTTTTTAAAGCGGATCTA 2596
QY 840 GAAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 899
Db 2597 GAAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 2656
QY 900 CTGAAGAAATAAGTCAGTGACCCAGAAAGACGGAAGATGGCTGGATAACTTTGCCCGGTGT 959
Db 2657 CTGAAGAAATAAGTCAGTGACCCAGAAAGACGGAAGATGGCTGGATAACTTTGCCCGGTGT 2716
QY 960 TGGGATAATTTAGTCCAAAAAACTTGAAAAGAGTACAGACAGACCCCTTGAAAAGACTCCAG 1019
Db 2717 TGGGATAATTTAGTCCAAAAAACTTGAAAAGAGTACAGACAGACCCCTTGAAAAGACTCCAG 2776
QY 1020 GAACCTCAAGAGGCCACCGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAG 1079
Db 2777 GAACCTCAAGAGGCCACCGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAG 2836
QY 1080 GGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAA 1139
Db 2837 GGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAA 2896
QY 1140 GTCAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAAGAGAACGTCGAGCCACGTCATGAC 1199
Db 2897 GTCAGGCACCTTCGAGGAGAAATTCGCCCTCTGAAAAGAGAACGTCGAGCCACGTCATGAC 2956
QY 1200 CTTGCTGCCAGCTTACCACCTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCACTCTG 1259
Db 2957 CTTGCTGCCAGCTTACCACCTTTGGGCATTTCAGCTCTCACCGTATAACCTCAGCACTCTG 3016
QY 1260 GAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGCCGAGTCAGGCAG 1319

RESULT 2
AAD37260
ID AAD37260 standard; DNA; 4414 BP.
XX
AC AAD37260;
XX
DT 21-AUG-2002 (first entry)
XX
DE Adeno-associated virus vector plasmid, AAV-MCK-3447.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-020077P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX
PT New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 65-66; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) promoter and a small polyA signal sequence
SQ Sequence 4414 BP; 1255 A; 1075 C; 1086 G; 998 T; 0 U; 0 Other;
Query Match 99.5%; Score 1990; DB 6; Length 4414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 60
Db 1757 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 1816
QY 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTAAT 120
Db 1817 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTAAT 1876
QY 121 GATGTGGAAGTGGTGAAGACCAGTTTTCATCTCATGAGGGGTACATGATGATTGACA 180
Db 1877 GATGTGGAAGTGGTGAAGACCAGTTTTCATCTACTCATGAGGGGTACATGATGATTGACA 1936
QY 181 GCCCATCAGGCCGGTGGTAAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240

Db 3017 GAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGACCGAGTCAGGCAG 3076
QY 1320 CTGCATGAAGCCCAAGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTGTC 1379
Db 3077 CTGCATGAAGCCCAAGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTGTC 3136
QY 1380 CAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAG 1439
Db 3137 CAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAG 3196
QY 1440 ACTCAAAACAACCTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTTTTAGCTGAC 1499
Db 3197 ACTCAAAACAACCTGCTGGGACCATCCCAAAATGACAGAGCTCTACCACTTTTAGCTGAC 3256
QY 1500 CTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGAAG 1559
Db 3257 CTGAATAATGTGAGATTTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGAAG 3316
QY 1560 GCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCTTGACCAACAAC 1619
Db 3317 GCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCTTGACCAACAAC 3376
QY 1620 CTCAAGCAAAATGACCAAGCCCATGGATATCTCTGAGATTTATTAATTTTGACCACTATT 1679
Db 3377 CTCAAGCAAAATGACCAAGCCCATGGATATCTCTGAGATTTATTAATTTTGACCACTATT 3436
QY 1680 TATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCTCTCTGCGTGGATATG 1739
Db 3437 TATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCTCTCTGCGTGGATATG 3496
QY 1740 TGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCCGTCTCTG 1799
Db 3497 TGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCCGTCTCTG 3556
QY 1800 TCTTTTAAACCTGGCATCATTTCCCTGTGTAAGCACATTTTGAAGACAAAGTACAGATAC 1859
Db 3557 TCTTTTAAACCTGGCATCATTTCCCTGTGTAAGCACATTTTGAAGACAAAGTACAGATAC 3616
QY 1860 CTTTTCAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCAGGCTGGCCCTCCTT 1919
Db 3617 CTTTTCAGCAAGTGGCAAGTTTCAACAGGATTTTGTGACCAAGCAGGCTGGCCCTCCTT 3676
QY 1920 CTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGAGT 1979
Db 3677 CTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGAGT 3736
QY 1980 AACATTGAGCCAAAGTGTCGGGA 2001
Db 3737 AACATTGAGCCAAAGTGTCGGGA 3758

RESULT 3
ID ABK81997
XX
AC ABK81997;
XX
DT 13-AUG-2002 (first entry)
XX
DE DNA encoding mini-dystrophin protein deltaR4-R23.
XX
KW Mini-dystrophin peptide; spectrin-like repeat domain; muscle disease;
KW Duchenne's muscular dystrophy; DMD; dystrophin; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200229056-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031126.
XX

PR 06-OCT-2000; 2000US-0238848P.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Chamberlain JS, Harper SQ;
XX
DR WPI; 2002-435334/46.
XX
PT A composition for preparing therapeutic drugs, has a mini-dystrophin
PT peptide comprising a specific number of spectrin-like repeat domains, or
PT a nucleic acid sequence encoding the mini-dystrophin peptide.
XX
PS Disclosure; Fig 12; 145pp; English.
XX
CC The invention describes a composition comprising a mini-dystrophin
CC peptide comprising a spectrin-like repeat domain, where the domain
CC comprises n spectrin-like repeats, and contains no more than n spectrin-
CC like repeats, where n is an even number between 4-24, or a nucleic acid
CC encoding a mini-dystrophin peptide. The mini-dystrophin peptide or the
CC polynucleotide encoding it is useful as a medicament, for preparing a
CC drug for therapeutic application and in the preparation of a composition
CC for treatment of muscle disease, e.g. Duchenne's muscular dystrophy
CC (DMD). This sequence represents a mini-dystrophin sequence of the
CC invention
XX
SQ Sequence 5417 BP; 1700 A; 1192 C; 1182 G; 1343 T; 0 U; 0 Other;
Query Match 91.0%; Score 1820.8; DB 6; Length 5417;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1999; Conservative 0; Mismatches 2; Indels 157; Gaps 2;
QY 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAGAA 60
Db 1199 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAGAA 1258
QY 61 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTCTTAAT 120
Db 1259 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTCTTAAT 1318
QY 121 GATGTGGAAGTGGTGAAGACCCAGTTTCATACTCATGAGGGTACATGATGGATTGACA 180
Db 1319 GATGTGGAAGTGGTGAAGACCCAGTTTCATACTCATGAGGGTACATGATGGATTGACA 1378
QY 181 GCCCATCAGGCGCGGTTGGTATATATTCTACAATTGGGAAGTAAAGCTGATTGGAACAGGA 240
Db 1379 GCCCATCAGGCGCGGTTGGTATATATTCTACAATTGGGAAGTAAAGCTGATTGGAACAGGA 1438
QY 241 AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCTAAATTCAAGA 300
Db 1439 AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCTAAATTCAAGA 1498
QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAGCAATTTACATAGAGTTTAAATG 360
Db 1499 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAGCAATTTACATAGAGTTTAAATG 1558
QY 361 GATCTCCAGAAATC-GAAACTGAAGAGATTGAATGACTGGCTAACAAAAACAGAGAAAGA 419
Db 1559 GATCTCCAGAAATCAGAAACTGAAGAGATTGAATGACTGGCTAACAAAAACAGAGAAAGA 1618
QY 420 ACAAGGAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAACCGCAAGTA 479
Db 1619 ACAAGGAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAACCGCAAGTA 1678
QY 480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAACAAAGTCAGGGTCAATTCTCTC 539
Db 1679 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAACAAAGTCAGGGTCAATTCTCTC 1738
QY 540 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTGGAA 599
Db 1739 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTGGAA 1798
QY 600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAGACCGC 659

Db 1799 GAACAACTTAAGGTATTGGGAGATCGATGGCAAAACATCTGTAGATCGACAGAAGACCGC 1858
QY TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCCTTACTGAAGAACAGTGCCTT 719
Db TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCCTTACTGAAGAACAGTGCCTT 1918
QY TTTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAGATTCAACAACCTGGCTTT 779
Db TTTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAGATTCAACAACCTGGCTTT 1978
QY AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTTAAAAAGCGGATCTA 839
Db AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTTAAAAAGCGGATCTA 2038
QY GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 899
Db GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 2098
QY CTGAAGAATAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT 959
Db CTGAAGAATAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT 2158
QY TGGGATAATTTAGTCCAAAAAATTGAAAAGAGTACAGCACAGA----- 1002
Db TGGGATAATTTAGTCCAAAAAATTGAAAAGAGTACAGCACAGATTTTCACAGGCTGTCAAC 2218
QY ----- 1002
Db ACCACTCAGCCATCACTAACACAGACAACTGTAATGGAACACAGTAACACTACGGTGACCACA 2278
QY ----- 1002
Db AGGGAACAGATCCTGGTAAAGCATGCTCAAGAGGAACTTCCACCACCACCTCCCCAAAAG 2338
QY -----CCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAG 1043
Db AAGAGGCAGATTACTGTGGATCTTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAG 2398
QY CTGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGAT 1103
Db CTGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGAT 2458
QY CTCCTCATTTGACTCTCTCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATT 1163
Db CTCCTCATTTGACTCTCTCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATT 2518
QY GCGCCTCTGAAAGAGAACGTGAGCCACGTCATGACCTTGCTCGCCAGCTTACCACCTTTG 1223
Db GCGCCTCTGAAAGAGAACGTGAGCCACGTCATGACCTTGCTCGCCAGCTTACCACCTTTG 2578
QY GGCATTGAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACAGATGGAAG 1283
Db GGCATTGAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACAGATGGAAG 2638
QY CTTCTGCAAGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCAAGGACTTT 1343
Db CTTCTGCAAGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCAAGGACTTT 2698
QY GGTCCAGCATCTCAGCACTTCTTTCCACGTCGTCCAGGGTCCCTGGGAGAGAGCCATC 1403
Db GGTCCAGCATCTCAGCACTTCTTTCCACGTCGTCCAGGGTCCCTGGGAGAGAGCCATC 2758
QY TCGCCAAACAAAGTCCCTACTATATCAACCACGAGACTCAACAACTTGTGGGACCAT 1463
Db TCGCCAAACAAAGTCCCTACTATATCAACCACGAGACTCAACAACTTGTGGGACCAT 2818
QY CCCAAATGACAGAGCTTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCT 1523
Db CCCAAATGACAGAGCTTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCT 2878
QY TATAGGACTGCCATGAACTCCGAAGACTGCAGAGGCCCTTTGCTTGATCTCTTTGAGC 1583
Db TATAGGACTGCCATGAACTCCGAAGACTGCAGAGGCCCTTTGCTTGATCTCTTTGAGC 2938

QY 1584 CTGTCAAGTGCATGTGATGCCTTGGACCAGCACAAACCTCAAGCAAAATGACCAGCCCATG 1643
Db CTGTCAAGTGCATGTGATGCCTTGGACCAGCACAAACCTCAAGCAAAATGACCAGCCCATG 2998
QY GATATCCTGCAGATTATTAATTTGTTGACCACACTATTTATGACCGCTGGAGCAAGAGCAC 1703
Db GATATCCTGCAGATTATTAATTTGTTGACCACACTATTTATGACCGCTGGAGCAAGAGCAC 3058
QY AACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTCTGAACTGGCTGCTGAATGTT 1763
Db AACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTCTGAACTGGCTGCTGAATGTT 3118
QY TATGATACGGGACGAAACAGGAGGATCCGTGTCCTCTTTTAAAACTGGCATCATTTCC 1823
Db TATGATACGGGACGAAACAGGAGGATCCGTGTCCTCTTTTAAAACTGGCATCATTTCC 3178
QY CTCTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCA 1883
Db CTCTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCA 3238
QY ACAGGATTTTGTGACCAGCGCAGGCTGGCCCTCTCTGTCATGATTTCTATCCAAATTTCCA 1943
Db ACAGGATTTTGTGACCAGCGCAGGCTGGCCCTCTCTGTCATGATTTCTATCCAAATTTCCA 3298
QY AGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGA 2001
Db AGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGA 3356

RESULT 4

AAD37240
ID AAD37240 standard; DNA; 3510 BP.
XX
AC AAD37240;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human dystrophin minigene delta3510.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX
PT New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 51-52; 71pp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control

QY 540 ACTCACAAGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGGAACACTGCTGCTTTGGAA 599
Db |||||
1735 ACTCACAAGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGGAACACTGCTGCTTTGGAA 1794
QY 600 GAACAACTTAAGGTATTGGGAGATCGATGGCAAAACATCTGTAGATGGAACAGACCCG 659
Db |||||
1795 GAACAACTTAAGGTATTGGGAGATCGATGGCAAAACATCTGTAGATGGAACAGACCCG 1854
QY 660 TGGGTTCTTTTACAAGACATCCTTCTCAATGGCAACGCTTTACTGAAGAACAGTGCCTT 719
Db |||||
1855 TGGGTTCTTTTACAAGACATCCTTCTCAATGGCAACGCTTTACTGAAGAACAGTGCCTT 1914
QY 720 TTTAGTGCATGGCTTTTCAGAAAAAGAGATGAGTGAACAAGATTACACAACTGGCTTT 779
Db |||||
1915 TTTAGTGCATGGCTTTTCAGAAAAAGAGATGAGTGAACAAGATTACACAACTGGCTTT 1974
QY 780 AAAGATCAAAATGAATGTTATCAAGTCTTCAAAAACTGGCCGTTTAAAAAGCGGATCTA 839
Db |||||
1975 AAAGATCAAAATGAATGTTATCAAGTCTTCAAAAACTGGCCGTTTAAAAAGCGGATCTA 2001
QY 840 GAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 899
Db ----- 2001
QY 900 CTGAAGAAATAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATACTTTGCCCGGTGT 959
Db ----- 2001
QY 1020 GAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCCAAGCTGAGGTGATCAAG 1079
Db ----- 2001
QY 1080 GGATCCTGGCAGCCCGTGGCGGATCTCCTCATTTGATCTCTCCAAGATCACCTCGAGAAA 1139
Db -----CTCGAGAAA 2010
QY 1140 GTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGCTGAGCCACGTCAATGAC 1199
Db |||||
2011 GTCAAGGCACCTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGCTGAGCCACGTCAATGAC 2070
QY 1200 CTGCTCGCCAGCTTACCACCTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTG 1259
Db |||||
2071 CTGCTCGCCAGCTTACCACCTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTG 2130
QY 1260 GAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCGCTGAGGACCGAGTCAGGCAG 1319
Db |||||
2131 GAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCGCTGAGGACCGAGTCAGGCAG 2190
QY 1320 CTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGCTCTGTC 1379
Db |||||
2191 CTGCATGAAGCCCAACAGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGCTCTGTC 2250
QY 1380 CAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCACGAG 1439
Db |||||
2251 CAGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTCCCTACTATATCAACCACGAG 2310
QY 1440 ACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGAC 1499
Db |||||
2311 ACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGAC 2370
QY 1500 CTGAATAATGTGAGATCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTCGAGAAG 1559
Db |||||
2371 CTGAATAATGTGAGATCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTCGAGAAG 2430
QY 1560 GCCCTTTGCTTGGATCTCTTGAGCCTGTGATGATGCTTGGACCGACCAAC 1619
Db |||||
2431 GCCCTTTGCTTGGATCTCTTGAGCCTGTGATGATGCTTGGACCGACCAAC 2490

QY 1620 CTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTACCACCTATT 1679
Db |||||
2491 CTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTACCACCTATT 2550
QY 1680 TATGACCGCCTGGAGCAAGAGACAAACAATTGGTCAACGCTCCCTCTCTGCTGGTGGATATG 1739
Db |||||
2551 TATGACCGCCTGGAGCAAGAGACAAACAATTGGTCAACGCTCCCTCTCTGCTGGTGGATATG 2610
QY 1740 TGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGATCCGTGCTCTG 1799
Db |||||
2611 TGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGAGATCCGTGCTCTG 2670
QY 1800 TCTTTTAAAACTGGCATCATCTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAGATAC 1859
Db |||||
2671 TCTTTTAAAACTGGCATCATCTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAGATAC 2730
QY 1860 CTTTTCAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGAGCTGGGCTCCTT 1919
Db |||||
2731 CTTTTCAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCAGCGAGCTGGGCTCCTT 2790
QY 1920 CTGCATGATTTCTATCCAAATTCGAAGACAGTTGGTGAAGTTGCATCCTTTGGGGCAGT 1979
Db |||||
2791 CTGCATGATTTCTATCCAAATTCGAAGACAGTTGGTGAAGTTGCATCCTTTGGGGCAGT 2850
QY 1980 AACATTGAGCCCAAGTGTCCGGA 2001
Db |||||
2851 AACATTGAGCCCAAGTGTCCGGA 2872

RESULT 7

AZ48567

ID AZ48567 standard; cDNA to mRNA; 4402 BP.

XX AZ48567;

XX 31-MAR-2000 (first entry)

DE A rod shortened dystrophin (deltaDysAx11) encoding nucleotide sequence.

XX Muscular dystrophy; rod domain; adeno-associated virus; AAV;

KW dystrophin gene; truncated; ds.

XX Homo sapiens.

PN JP11318467-A.

PD 24-NOV-1999.

PF 08-MAY-1998; 98JP-00142134.

XX 08-MAY-1998; 98JP-00142134.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

DR WPI; 2000-100771/09.

DR P-PSDB; AAY59238.

XX A gene encoding a shortened dystrophin - useful for the treatment of

PT muscular dystrophy.

XX Claim 7; Page 16-17; 44pp; Japanese.

PS The invention provides a gene for the treatment of muscular dystrophy
XX having at least one rod repeat structure of hinge 1, hinge 4 and rod
CC domain of dystrophin gene and having a base sequence of 4.5 kb. The gene
CC and a gene-introducing medium consisting of an adeno-associated virus
CC (AAV) vector or lentivirus vector containing the rod shortened dystrophin
CC genes can be used for the genetic treatment of muscular dystrophy of low
CC immune reaction. The present sequence represents a rod shortened
CC dystrophin encoding sequence

SQ Sequence 4402 BP; 1329 A; 1000 C; 1019 G; 1054 T; 0 U; 0 Other;

		Query Match	63.4%;	Score 1269.2;	DB 3;	Length 4402;		
		Best Local Similarity	82.1%;	Pred. No. 0;				
		Matches 1644;	Conservative 0;	Mismatches 33;	Indels 325;	Gaps 3;		
QY	1	GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA	60					
Db	1195	GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA	1254					
QY	61	GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT	120					
Db	1255	GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT	1314					
QY	121	GATGTGGAAGTGGTGAAGAACCAAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA	180					
Db	1315	GATGTGGAAGTGGTGAAGAACCAAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA	1374					
QY	181	GCCCATCAGGGCCGGTGGTAAATATTCTACAATTGCGAAGTAAGCTGATTGGAACAGGA	240					
Db	1375	GCCCATCAGGGCCGGTGGTAAATATTCTACAATTGCGAAGTAAGCTGATTGGAACAGGA	1434					
QY	241	AAATTATCAGAAGATGAAGAAAACCTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA	300					
Db	1435	AAATTATCAGAAGATGAAGAAAACCTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA	1494					
QY	301	TGGGAATGCCTCAGGCTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG	360					
Db	1495	TGGGAATGCCTCAGGCTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG	1554					
QY	361	GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTTAACAAAAACAGAAAGAA	419					
Db	1555	GATCTCCAGAATCAGAAAACCTGAAAGAGTTGAATGACTGGCTTAACAAAAACAGAAAGAA	1614					
QY	420	ACAAGGAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTTAAACCGCAAGTA	479					
Db	1615	ACAAGGAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTTAAACCGCAAGTA	1674					
QY	480	CAACAACATAAGGTGCTTCAAGAAAGATCTAGAAACAAGTAACAAGTCAAGTCAATTCTCTC	539					
Db	1675	CAACAACATAAGGTGCTTCAAGAAAGATCTAGAAACAAGTAACAAGTCAAGTCAATTCTCTC	1734					
QY	540	ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCAGCAACTGCTGCTTTGGAA	599					
Db	1735	ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCAGCAACTGCTGCTTTGGAA	1794					
QY	600	GAACAACCTTAAGGTATTTGGGAGATCGATGGGCAACATCTGTAGATGGACAGAGACCGC	659					
Db	1795	GAACAACCTTAAGGAGTCAATACTAGTGGGAAAA-----	1829					
QY	660	TGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGCTCTTACTGAAGAACAGTGCCTT	719					
Db	1830	-----	1829					
QY	720	TTTAGTGATGGCTTTCAGAAAAAGAAAGATGCAGTGAACAAGATTACACAACTGGCTTT	779					
Db	1830	-----	1829					
QY	780	AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAAACCTGGCCGTTTTTAAAGCGGATCTA	839					
Db	1830	-----	1829					
QY	840	GAAAAGAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA	899					
Db	1830	-----	1829					
QY	900	CTGAAGAAATAAGTCAGTGACCCAGAAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT	959					
Db	1830	-----ATTGAACCTGCACTCCGCTGACTGGCAGAGAAA-----	1862					
QY	960	TGGGATAATTAGTCCAAAAACTTGAAAAAGAGTACAGCACAGACCCCTTGAAAAGACTCCAG	1019					
Db	1863	-----AATAGATGAGACCCCTTGAAAAGACTCCAG	1890					

QY	1020	GAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGTGAGGTGATCAAG	1079
Db	1891	GAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGTGAGGTGATCAAG	1950
QY	1080	GGATCTGGCAGCCGCTGGGCGATCTCTCTCAATGACTCTCTCCAAAGTACACCTCGAGAAA	1139
Db	1951	GGATCTGGCAGCCGCTGGGCGATCTCTCTCAATGACTCTCTCCAAAGTACACCTCGAGAAA	2010
QY	1140	GTCAAGGCACCTTCGAGGAGAAAATTGGCGCTCTGAAAGAGAACGTCGAGCCACGTCATGAC	1199
Db	2011	GTCAAGGCACCTTCGAGGAGAAAATTGGCGCTCTGAAAGAGAACGTCGAGCCACGTCATGAC	2070
QY	1200	CTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCACTCTG	1259
Db	2071	CTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCACTCTG	2130
QY	1260	GAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG	1319
Db	2131	GAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG	2190
QY	1320	CTGCATGAAGCCCAACAGGACTTTTGGTCCAGCATCTCAGCACTTTTCCACGCTCTGTC	1379
Db	2191	CTGCATGAAGCCCAACAGGACTTTTGGTCCAGCATCTCAGCACTTTTCCACGCTCTGTC	2250
QY	1380	CAGGTCCTGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAG	1439
Db	2251	CAGGTCCTGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAG	2310
QY	1440	ACTCAAAACAACCTTGTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGCTGAC	1499
Db	2311	ACTCAAAACAACCTTGTGGGACCATCCCAAAATGACAGAGCTCTACCACTCTTTAGCTGAC	2370
QY	1500	CTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGAAG	1559
Db	2371	CTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAGAAG	2430
QY	1560	GCCCTTTGCTTGGATCTCTTGAGCCTGTGAGTGCATGTGATGCGCTTGGACCAACAAC	1619
Db	2431	GCCCTTTGCTTGGATCTCTTGAGCCTGTGAGTGCATGTGATGCGCTTGGACCAACAAC	2490
QY	1620	CTCAAGCAAAATGACCCAGCCCATGGATATCTGCAGATTATTAATTTGACCACTATT	1679
Db	2491	CTCAAGCAAAATGACCCAGCCCATGGATATCTGCAGATTATTAATTTGACCACTATT	2550
QY	1680	TATGACCGCTGGAGCAAGAGCACAACAATTTGGTCAACGCTCCCTCTCTGCGTGGATATG	1739
Db	2551	TATGACCGCTGGAGCAAGAGCACAACAATTTGGTCAACGCTCCCTCTCTGCGTGGATATG	2610
QY	1740	TGTCTGAAGTGGCTGTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTCCTCTG	1799
Db	2611	TGTCTGAAGTGGCTGTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTCCTCTG	2670
QY	1800	TCCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACAATTTGGAAGACAAGTACAGATAC	1859
Db	2671	TCCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACAATTTGGAAGACAAGTACAGATAC	2730
QY	1860	CTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGGAGGCTGGGCCCTCTT	1919
Db	2731	CTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGGAGGCTGGGCCCTCTT	2790
QY	1920	CTGCATGATTTCTATCCAAATTCGAAGACAGTTGGGTGAAGTTGCATCTCTTTGGGGCAGT	1979
Db	2791	CTGCATGATTTCTATCCAAATTCGAAGACAGTTGGGTGAAGTTGCATCTCTTTGGGGCAGT	2850
QY	1980	AACATTGAGCCAAAGTGTCCGGA	2001
Db	2851	AACATTGAGCCAAAGTGTCCGGA	2872

AC AAD37237;
XX DT 21-AUG-2002 (first entry)
XX Human dystrophin minigene delta3849.
XX DE
XX Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX OS Homo sapiens.
XX WO200183695-A2.
XX PN
XX PD 08-NOV-2001.
XX 27-APR-2001; 2001WO-US013677.
XX PF
XX PR 28-APR-2000; 2000US-0200777P.
XX (XIAO/) XIAO X.
XX PA
XX PI Xiao X;
XX WPI; 2002-049342/06.
DR
XX New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
XX Example 1; Page 48-49; 71pp; English.
XX
XX The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is human
CC dystrophin minigene delta3849 containing nucleotides 1-1668 (N-terminus,
CC hinge H1 and rods R1, R2), 8059-10227 (rods R22, R23 and R24, hinge H4
CC and CR domain) and 11047-11058 (dystrophin last 3 amino acids)
XX
SQ Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 U; 0 Other;

Query Match 63.1%; Score 1263; DB 6; Length 3858;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1816; Conservative 0; Mismatches 185; Indels 412; Gaps 3;

QY 1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 60
DB |||||||
1000 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 1059

QY 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTTAAT 120
DB |||||||
1060 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTTAAT 1119

QY 121 GATGTGGAAGTGGTGAAGAACCCAGTTTCATACTCATGAGGGGTACATGATGGATTGACA 180
DB |||||||
1120 GATGTGGAAGTGGTGAAGAACCCAGTTTCATACTCATGAGGGGTACATGATGGATTGACA 1179

QY 181 GCCCATCAGGCCCGGGTTGGTAATATTTCTACAATTGGGAAGTAAAGCTGATTGGAACAGGA 240
DB |||||||
1180 GCCCATCAGGCCCGGGTTGGTAATATTTCTACAATTGGGAAGTAAAGCTGATTGGAACAGGA 1239

QY 241 AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 300
DB |||||||
1240 AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 1299

QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAACAAACAAAGCAATTTACATAGAGTTTAAATG 360
DB |||||||
1300 TGGGAATGCCTCAGGGTAGCTAGCATGGAACAAACAAAGCAATTTACATAGAGTTTAAATG 1359

QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAAACAAAACAGAGAAAGA 419
DB |||||||
1360 GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAAACAAAACAGAGAAAGA 1419

QY 420 ACAAGGAAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTAAACGCGCAAGTA 479
DB |||||||
1420 ACAAGGAAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTAAACGCGCAAGTA 1479

QY 480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAAACAAGTCAGGGTCAATTCTCTC 539
DB |||||||
1480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAAACAAGTCAGGGTCAATTCTCTC 1539

QY 540 ACTACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
DB |||||||
1540 ACTACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 1599

QY 600 GAACAACCTTAAGGTATTGGAGATCGATGGGCAACAATCTGTAGATGGACAGAACACCGC 659
DB |||||||
1600 GAACAACCTTAAGGTATTGGAGATCGATGGGCAACAATCTGTAGATGGACAGAACACCGC 1659

QY 660 TGGTTCCTTTTACAAGACATCCTTCTCAAATGGCAACCTTACTGGAAGAACAGTGCCTT 719
DB |||||||
1660 TGGTTCCTTTTACAAGACATCATAAGATTACTGCAACAGTTCCTCCCTGGACCTGGAAGAAG 1719

QY 720 TTTAGTGCATGGCTTTTACAGAAAAAGAAAGATGCAGTGAACAAGATTACACAACTGGCTTT 779
DB |||||||
1720 TTTCTTGCCTGGCTTACAGAAAGCTGAAACAACTGCCAATGTCTCTACAGGATGCTACCCGT 1779

QY 780 A-----AAGATCAAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTT 824
DB |||||||
1780 AAGGAAAGGCTCCTAGAAAGACTCCAAGGGAGTAAAGAGTGAATAAACAATGGCAAGAC 1839

QY 825 TTAAGAAGCGGATCTAGAAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACA 884
DB |||||||
1840 CTCCAAGGTGAATTTGAAGTCTCACAGATGTTTATCAACAACCTGGATGAAAAACAGCCAA 1899

QY 885 GATCTTCTTTCAACACTGAAGATAAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGAT 944
DB |||||||
1900 AAATCTCTGAGATCCCTGGAGGTTCCGATGATGCAGTCTGTGTACAAAGACGTTTGGAT 1959

QY 945 AACTTTGCCCGGTGTTGGGATAATTAGTCCAAAAACCTTGAAAAAGAGTACAGCAC----- 999
DB |||||||
1960 AACATGAACCTCAAGTGGAGTGAACCTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTG 2019

QY 1000 ----- 999
DB
QY 2020 GAAGCCAGTCTGACCAGTGGAGCGCTCTGCACCTTTCTCTGCAGGAACCTTCTGGTGTG 2079
DB ----- 999
QY 2080 CTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGGACTTTCCAGCA 2139
DB ----- 999
QY 2140 GTTCAGAAAGCAACGATGTACATAGGGCCTTCAAGAGGGGAATTGAAAAACTAAAGAACCT 2199
DB ----- 999
QY 2200 GTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGAGCCCTTTGGAAGGA 2259
DB ----- 999
QY 2260 CTAGAGAAACTCTACCAGGAGCCCGAGAGAGTGCCTCTCTGAGGAGAGAGCCAGAAATGTC 2319
DB ----- 999
QY 2320 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAAAAATTGAACCTG 2379
DB -----
QY 1000 -----AGACCTTTGAAAGACTCCAGGAACCTTCAA 1028

Db	2380	CACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCTTTGAAAGACTCCAGAACTTCAA	2439
Qy	1029	GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGATCAAGGGATCCTGG	1088
Db	2440	GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGATCAAGGGATCCTGG	2499
Qy	1089	CAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCA	1148
Db	2500	CAGCCCGTGGCGGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCA	2559
Qy	1149	CTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGC	1208
Db	2560	CTTCGAGGAGAAATTGGCGCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGC	2619
Qy	1209	CAGCTTACCACCTTTGGGCAATTCAGCTCTCAACGATATAACCTCAGCACTCTGGAAGACCTG	1268
Db	2620	CAGCTTACCACCTTTGGGCAATTCAGCTCTCAACGATATAACCTCAGCACTCTGGAAGACCTG	2679
Qy	1269	AACACCAGATGGAAGCTTTCAGGTGGCCGTCGAGGACCGAGTCAGCAGCTGCATGAA	1328
Db	2680	AACACCAGATGGAAGCTTTCAGGTGGCCGTCGAGGACCGAGTCAGCAGCTGCATGAA	2739
Qy	1329	GCCACAGGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCTGTCCAGGGTCCC	1388
Db	2740	GCCACAGGGACTTTGGTCCAGCATCTCAGCACTTCTTTCCACGTCTGTCCAGGGTCCC	2799
Qy	1389	TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACACGAGACTCAAAACA	1448
Db	2800	TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACACGAGACTCAAAACA	2859
Qy	1449	ACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT	1508
Db	2860	ACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT	2919
Qy	1509	GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTCCAGAAAGGCCCTTGC	1568
Db	2920	GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTCCAGAAAGGCCCTTGC	2979
Qy	1569	TTGGATCTCTTGAGCCTGTGAGCTGATGATGCTTGGACCAAGCAACCTCAAGCAA	1628
Db	2980	TTGGATCTCTTGAGCCTGTGAGCTGATGATGCTTGGACCAAGCAACCTCAAGCAA	3039
Qy	1629	AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCACTATTTATGACCGC	1688
Db	3040	AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCACTATTTATGACCGC	3099
Qy	1689	CTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAAC	1748
Db	3100	CTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAAC	3159
Qy	1749	TGGCTGCTGAATGTTTATGATACGGGACCAACAGGGAGGATCCGTGCTCTTTTAAA	1808
Db	3160	TGGCTGCTGAATGTTTATGATACGGGACCAACAGGGAGGATCCGTGCTCTTTTAAA	3219
Qy	1809	ACTGGCATATTTCCTGTGTAAAGCACATTTGGAAGACAACTACAGATACCTTTTCAAG	1868
Db	3220	ACTGGCATATTTCCTGTGTAAAGCACATTTGGAAGACAACTACAGATACCTTTTCAAG	3279
Qy	1869	CAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCTGGCCCTCCTTCTGATGAT	1928
Db	3280	CAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGCTGGCCCTCCTTCTGATGAT	3339
Qy	1929	TCTATCCAAATCCAAAGACAGTTGGTGAAGTTGCATCTTTTGGGGCAGTAACATTGAG	1988
Db	3340	TCTATCCAAATCCAAAGACAGTTGGTGAAGTTGCATCTTTTGGGGCAGTAACATTGAG	
Qy	1989	CCAAGTGTCCGGA 2001	
Db	3400	CCAAGTGTCCGGA 3412	

AAD37257	
ID	AAD37257 standard; DNA; 4825 Bp.
XX	
AC	AAD37257;
XX	
DT	21-AUG-2002 (first entry)
XX	
DE	Adeno-associated virus vector plasmid, AAV-MCK-delta3849.
XX	
KW	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW	adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW	Becker muscular dystrophy; ds.
XX	
OS	Homo sapiens.
OS	Unidentified.
OS	Chimeric.
XX	
PN	WO200183695-A2.
XX	
PD	08-NOV-2001.
XX	
PF	27-APR-2001; 2001WO-US013677.
XX	
PR	28-APR-2000; 2000US-0200777P.
XX	
PA	(XIAO/) XIAO X.
XX	
PI	Xiao X;
XX	
DR	WPI; 2002-049342/06.
XX	
PT	New dystrophin minigene for treating Duchenne or Becker muscular
PT	dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT	rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT	gene.
XX	
PS	Example 1; Page 61-62; 71pp; English.
XX	
CC	The present invention relates to an isolated nucleotide sequence encoding
CC	a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC	terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC	domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC	invention also relates to a recombinant adeno-associated virus (AAV)
CC	comprising dystrophin minigene operably linked to an expression control
CC	element. The dystrophin minigene in operable linkage with an expression
CC	control element, in a recombinant adeno-associated virus or retrovirus is
CC	useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC	dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC	vector plasmid construct containing human dystrophin minigenes, a muscle
CC	creatine kinase (MCK) promoter and a small polyA signal sequence
XX	
SQ	Sequence 4825 Bp; 1369 A; 1175 C; 1204 G; 1077 T; 0 U; 0 Other;
	Query Match 63.1%; Score 1263; DB 6; Length 4825;
	Best Local Similarity 75.3%; Pred. No. 0;
	Matches 1816; Conservative 0; Mismatches 185; Indels 412; Gaps 3;
QY	1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACACAGCTTTAGAGAA 60
Db	1757 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACACAGCTTTAGAGAA 1816
QY	61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTTAAT 120
Db	1817 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTTAAT 1876
QY	121 GATGTGGAAGTGGTGAAGAACACAGTTTTCATCTCATAGGGGTACATGATGGATTGACA 180
Db	1877 GATGTGGAAGTGGTGAAGAACACAGTTTTCATCTCATAGGGGTACATGATGGATTGACA 1936
QY	181 GCCCATCAGGGCCGGTTGGTGAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db	1937 GCCCATCAGGGCCGGTTGGTGAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 1996


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Db      4157 CCAAGTGTCCGGA 4169

RESULT 10
AAD37263
ID      AAD37263 standard; DNA; 4848 BP.
XX
AC      AAD37263;
XX
DT      21-AUG-2002 (first entry)
XX
DE      Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849.
XX
KW      Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW      adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW      Becker muscular dystrophy; ds.
XX
OS      Homo sapiens.
OS      Cytomegalovirus.
OS      Unidentified.
OS      Chimeric.
XX
PN      WO200183695-A2.
XX
PD      08-NOV-2001.
XX
PF      27-APR-2001; 2001WO-US013677.
XX
PR      28-APR-2000; 2000US-0200777P.
XX
PA      (XIAO/) XIAO X.
XX
PI      Xiao X;
XX
WPI; 2002-049342/06.
XX

New dystrophin minigene for treating Duchenne or Becker muscular
dystrophy comprises an N-terminal domain or modified N-terminal domain,
rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
gene.

Example 1; Page 68-70; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding
a dystrophin minigene. The minigene comprises N-terminal or modified N-
terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
domains and cysteine-rich domains of dystrophin or utrophin genes. The
invention also relates to a recombinant adeno-associated virus (AAV)
comprising dystrophin minigene operably linked to an expression control
element. The dystrophin minigene in operable linkage with an expression
control element, in a recombinant adeno-associated virus or retrovirus is
useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
dystrophy (BMD) in a mammalian subject. The present sequence is AAV
vector plasmid construct containing human dystrophin minigenes, a
cytomegalovirus (CMV) promoter and a small polyA signal sequence

Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 U; 0 Other;

Query Match      63.1%; Score 1263; DB 6; Length 4848;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1816; Conservative 0; Mismatches 185; Indels 412; Gaps 3;

QY      1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 60
      |||
Db      1780 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 1839

QY      61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAGGAGAGATTCTTAAT 120
      |||
Db      1840 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAGGAGAGATTCTTAAT 1899

QY      121 GATGTGGAAGTGGTGAAGAAGACCAGTTTCATCTCATGAGGGGTACATGATGGATTGACA 180
      |||
Db      1900 GATGTGGAAGTGGTGAAGAAGACCAGTTTCATCTCATGAGGGGTACATGATGGATTGACA 1959

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QY 1000 ----- 999
Db 3040 CTAGAGAACTCTACCAGGAGCCACAGAGAGCTGCCTCCTGAGGAGAGAGCCAGAAATGTC 3099
QY 1000 ----- 999
Db 3100 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAAAATTGAACCTG 3159
QY 1000 -----AGACCTTTGAAAGACTCCAGGAACCTTCAA 1028
Db 3160 CACTCCGCTGACTGGCAGAGAAAAAATAGATGAGACCTTTGAAAGACTCCAGGAACCTTCAA 3219
QY 1029 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGATCAAGGGATCCTGG 1088
Db 3220 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGATCAAGGGATCCTGG 3279
QY 1089 CAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGAAAAAGTCAAGGCA 1148
Db 3280 CAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGAAAAAGTCAAGGCA 3339
QY 1149 CTTCGAGGAGAAATTGGCCCTCTCTGAAAGAGAACGTGAGCCACGTCATGACCTTGCTCGC 1208
Db 3340 CTTCGAGGAGAAATTGGCCCTCTCTGAAAGAGAACGTGAGCCACGTCATGACCTTGCTCGC 3399
QY 1209 CAGCTTACCACCTTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 1268
Db 3400 CAGCTTACCACCTTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 3459
QY 1269 AACACAGATGGAAGCTTCTGCAGGTGGCCGTGAGGACCGAGTCAGGAGCTGCATGAA 1328
Db 3460 AACACAGATGGAAGCTTCTGCAGGTGGCCGTGAGGACCGAGTCAGGAGCTGCATGAA 3519
QY 1329 GCCCACAGGGACTTTTGGTCCAGCATCTCAGCACTTCTTTCCACGCTCTGCCAGGTTCCC 1388
Db 3520 GCCCACAGGGACTTTTGGTCCAGCATCTCAGCACTTCTTTCCACGCTCTGCCAGGTTCCC 3579
QY 1389 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACA 1448
Db 3580 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACA 3639
QY 1449 ACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGCTTTTAGCTGACCTGAATAAT 1508
Db 3640 ACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGCTTTTAGCTGACCTGAATAAT 3699
QY 1509 GTCAGATTCTCAGCTTATAGACTGCCATGAACTCCGAAGACTGCAGAAGGCCCTTTGC 1568
Db 3700 GTCAGATTCTCAGCTTATAGACTGCCATGAACTCCGAAGACTGCAGAAGGCCCTTTGC 3759
QY 1569 TTGGATCTCTTGAGCCTGTACAGTGCATGTGATGCCTTGGACCAGCACAACTCAAGCAA 1628
Db 3760 TTGGATCTCTTGAGCCTGTACAGTGCATGTGATGCCTTGGACCAGCACAACTCAAGCAA 3819
QY 1629 AATGACAGAGCCATGATATCCTGCAGATTATTAATTGTTGACCACTATTTATGACCCG 1688
Db 3820 AATGACAGAGCCATGATATCCTGCAGATTATTAATTGTTGACCACTATTTATGACCCG 3879
QY 1689 CTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGTGAAC 1748
Db 3880 CTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGTGAAC 3939
QY 1749 TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCTCTTTTAAA 1808
Db 3940 TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCTCTTTTAAA 3999
QY 1809 ACTGGCATATTTCCCTGTGTAAGACACATTTTGGAGACAAAGTACAGATACCTTTTCAAG 1868
Db 4000 ACTGGCATATTTCCCTGTGTAAGACACATTTTGGAGACAAAGTACAGATACCTTTTCAAG 4059
QY 1869 CAAGTGGCAAGTTCAACAGGATTTTGACAGCGCAGGCTGGGCCCTCCTTCTGTCATGAT 1928
Db 4060 CAAGTGGCAAGTTCAACAGGATTTTGACAGCGCAGGCTGGGCCCTCCTTCTGTCATGAT 4119
QY 1929 TCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAG 1988

Db 4120 TCTATCCAAATTCGAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGCAGTAACATTGAG 4179
QY 1989 CCAAGTGTCCGGA 2001
Db 4180 CCAAGTGTCCGGA 4192
RESULT 11
AAD37264
ID AAD37264 standard; DNA; 5060 BP.
XX
AC AAD37264;
XX
DT 21-AUG-2002 (first entry)
XX
DE Adeno-associated virus (AAV) vector plasmid, AAV-E-CMV-3849.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
OS Cytomegalovirus.
OS Unidentified.
OS Chimeric.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX
PT New dystrophin minigene for treating Duchenne or Becker muscular
PT dystrophy comprises an N-terminal domain or modified N-terminal domain,
PT rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
PT gene.
XX
PS Example 1; Page 70-71; 7lpp; English.
XX
CC The present invention relates to an isolated nucleotide sequence encoding
CC a dystrophin minigene. The minigene comprises N-terminal or modified N-
CC terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4
CC domains and cysteine-rich domains of dystrophin or utrophin genes. The
CC invention also relates to a recombinant adeno-associated virus (AAV)
CC comprising dystrophin minigene operably linked to an expression control
CC element. The dystrophin minigene in operable linkage with an expression
CC control element, in a recombinant adeno-associated virus or retrovirus is
CC useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular
CC dystrophy (BMD) in a mammalian subject. The present sequence is AAV
CC vector plasmid construct containing human dystrophin minigenes, a muscle
CC creatine kinase (MCK) enhancer, a cytomegalovirus (CMV) promoter and a
CC small polyA signal sequence
XX
SQ Sequence 5060 BP; 1449 A; 1217 C; 1234 G; 1160 T; 0 U; 0 Other;

Query Match 63.1%; Score 1263; DB 6; Length 5060;
Best Local Similarity 75.3%; Pred.No. 0;
Matches 1816; Conservative 0; Mismatches 185; Indels 412; Gaps 3;
QY 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACAGCTTTAGAGAA 60
Db 1992 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACAGCTTTAGAGAA 2051
QY 61 GTATTATCGTGGCTTCTTTCTGTGTGAGGACACATTGCAAGCACAGGAGAGATTCTTAAT 120

Db 2052 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAAGGAGATTCTTAAT 2111
QY 121 GATGTGGAAGTGGTGAAGACCAAGTTTCATACTCATGAGGGGTACATGATGATTTGACA 180
Db 2112 GATGTGGAAGTGGTGAAGACCAAGTTTCATACTCATGAGGGGTACATGATGATTTGACA 2171
QY 181 GCCCATCAGGGCCGGGTTGGTAAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 2172 GCCCATCAGGGCCGGGTTGGTAAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA 2231
QY 241 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTTAAATTCAGA 300
Db 2232 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTTAAATTCAGA 2291
QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGATTTTAATG 360
Db 2292 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGATTTTAATG 2351
QY 361 GATCTCCAGAAATC-GAAACTGAAAGAGTTGAATGACTGGCTAAACAAAAACAGAAAGAA 419
Db 2352 GATCTCCAGAAATCAGAAACTGAAAGAGTTGAATGACTGGCTAAACAAAAACAGAAAGAA 2411
QY 420 ACAAGGAAATGAGGAAGAGCCTCTTTGGACCTGATCTTGAAGACCTTAAACGCCAAGTA 479
Db 2412 ACAAGGAAATGAGGAAGAGCCTCTTTGGACCTGATCTTGAAGACCTTAAACGCCAAGTA 2471
QY 480 CAACAACATAAGGTGCTTCAAGAAAGATCTAGAACAAAGAACAAAGTCAAGGTCAATTCCTC 539
Db 2472 CAACAACATAAGGTGCTTCAAGAAAGATCTAGAACAAAGAACAAAGTCAAGGTCAATTCCTC 2531
QY 540 ACTCACATGGTGGTAGTTGATGAATCTAGTGGCAACATCTGTAGATGGACAGAACCCG 659
Db 2532 ACTCACATGGTGGTAGTTGATGAATCTAGTGGCAACATCTGTAGATGGACAGAACCCG 2591
QY 600 GAACAACTTAAGGTATTTGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCG 659
Db 2592 GAACAACTTAAGGTATTTGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCG 2651
QY 660 TGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGTCTTACTGAAGAACAGTGCCCT 719
Db 2652 TGGGTTCTTTTACAAGACATCCTCATAGATTACTGCAACAGTTCCCTGACCTGGAAAAAG 2711
QY 720 TTTAGTGATGGCTTTTCAAGAAAAGAAAGATCGATGGAACAAAGATTCACACAACTGGCTTT 779
Db 2712 TTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCTCTACAGGATGCTACCCGT 2771
QY 780 A-----AAGATCAAAATGAATGTTTATCAAGTCTTCAAAACTGGCCGTT 824
Db 2772 AAGGAAAGSCTCTAGAAAGACTCCAGGGAGTAAAGAGCTGATGAACAATGGCAAGAC 2831
QY 825 TTAAAGCGGATCTAGAAAAGAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACA 884
Db 2832 CTCCAAGGTGAATGAAGCTCACACAGATGTTTATCAACAACTGGATGAAACACAGCCAA 2891
QY 885 GATCTTCTTCAACACTGAAGAAATAGTCAGTGACCCAGAAAGACGGAAGCATGGCTGGAT 944
Db 2892 AAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCTCTGTTTACAAAGACGTTGGAT 2951
QY 945 AACTTTGCCGGTGTGGGATAATTAGTCCAAAACTTGAAGAGTACAGCAC----- 999
Db 2952 AACATGAATTCAGTGGAGTGAATTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTG 3011
QY 1000 ----- 999
Db 3012 GAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTTTCTCTGCAGGAACCTTCTGGTGG 3071
QY 1000 ----- 999
Db 3072 CTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGCGGACTTTCCAGCA 3131
QY 1000 ----- 999

Db 3132 GTTCAGAAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCT 3191
QY 1000 ----- 999
Db 3192 GTAATCATGAGTACTCTTGAGACTGTACGAATAATTCTTGACAGAGCAGCCTTTGGAAGGA 3251
QY 1000 ----- 999
Db 3252 CTAGAGAAACTCTACCAGAGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCAGAAATGTC 3311
QY 1000 ----- 999
Db 3312 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTAGTGGGAAAAAATTGAACCTG 3371
QY 1000 -----AGACCCCTTGAAGACTCCAGGAACTTCAA 1028
Db 3372 CACTCCGCTGACTGSCAGAGAAAAATAGATGAGACCCCTTGAAGACTCCAGGAACTTCAA 3431
QY 1029 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAAGGGATCCTGG 1088
Db 3432 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAAGGGATCCTGG 3491
QY 1089 CAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCTCAAGATCACTCTGAGAAAAAGTCAAGGCA 1148
Db 3492 CAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCTCAAGATCACTCTGAGAAAAAGTCAAGGCA 3551
QY 1149 CTTGAGGAGAAATTGGCCCTCTGAAAGAGAACGCTGAGCCACGTCATGACCTTGTCTCGC 1208
Db 3552 CTTGAGGAGAAATTGGCCCTCTGAAAGAGAACGCTGAGCCACGTCATGACCTTGTCTCGC 3611
QY 1209 CAGCTTACCATTGTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 1268
Db 3612 CAGCTTACCATTGTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 3671
QY 1269 AACACCAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAGGCAGCTGCATGAA 1328
Db 3672 AACACCAGATGGAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAGGCAGCTGCATGAA 3731
QY 1329 GCCCACAGGACTTGGTCCAGCATCTCAGCACTCTCAGCACTTCTTTCCACGTCCTGTCCAGGTC 1388
Db 3732 GCCCACAGGACTTGGTCCAGCATCTCAGCACTCTCAGCACTTCTTTCCACGTCCTGTCCAGGTC 3791
QY 1389 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCCACGAGACTCAAAACA 1448
Db 3792 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCCACGAGACTCAAAACA 3851
QY 1449 ACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 1508
Db 3852 ACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 3911
QY 1509 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGABAGACTGCAGAAAGGCCCTTTGC 1568
Db 3912 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGABAGACTGCAGAAAGGCCCTTTGC 3971
QY 1569 TTGGATCTCTTGAGCCTGTGAGCTGTCATGTGATGCCCTTGACCCAGCACAACTCAAGCAA 1628
Db 3972 TTGGATCTCTTGAGCCTGTGAGCTGTCATGTGATGCCCTTGACCCAGCACAACTCAAGCAA 4031
QY 1629 AATGACCAGCCCATGGATATCTCTGAGATTATTAATTGTTTGACCACTATTTATGACCCG 1688
Db 4032 AATGACCAGCCCATGGATATCTCTGAGATTATTAATTGTTTGACCACTATTTATGACCCG 4091
QY 1689 CTGGACCAAGAGCACAAACAATTTGGTCAACGTCCCTCTCTGCTGGATATGTGTCTGAAC 1748
Db 4092 CTGGACCAAGAGCACAAACAATTTGGTCAACGTCCCTCTCTGCTGGATATGTGTCTGAAC 4151
QY 1749 TGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCTGTCTTTTAA 1808
Db 4152 TGGCTGCTGAATGTTTATGATACGGGACGAAACAGGAGGATCCGTGTCTGTCTTTTAA 4211
QY 1809 ACTGGCATCATTTCCCTGTAAAGCACATTTTGGAAAGCAAGTACAGATACCTTTTCAAG 1868
Db 4212 ACTGGCATCATTTCCCTGTAAAGCACATTTTGGAAAGCAAGTACAGATACCTTTTCAAG 4271

QY 1716 AACGTCCTCTCTGCGTGGATATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGA 1775
Db ||||| AACGTCCTCTCTGCGTGGATATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGA 3616
QY 1776 CGAACAGGGAGGATCCGTGTCCTGTCCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA 1835
Db ||||| CGAACAGGGAGGATCCGTGTCCTGTCCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA 3676
QY 1836 CATTGGAAGACAACTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGT 1895
Db ||||| CATTGGAAGACAACTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGT 3736
QY 1896 GACCAGCGCAGGCTGGGCCTCCTTCTGCAATGATTTCTATCCAAATTCCAAGACAGTTGGGT 1955
Db ||||| GACCAGCGCAGGCTGGGCCTCCTTCTGCAATGATTTCTATCCAAATTCCAAGACAGTTGGGT 3796
QY 1956 GAAGTTGCATCCTTTGGGGCAGTAACATTGAGCCAAAGTGTCGGGA 2001
Db ||||| GAAGTTGCATCCTTTGGGGCAGTAACATTGAGCCAAAGTGTCGGGA 3842

RESULT 15
AAD37230
ID AAD37230 standard; DNA; 4182 BP.
XX
AC AAD37230;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human dystrophin minigene delta4173.
XX
KW Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
KW adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
KW Becker muscular dystrophy; ds.
XX
OS Homo sapiens.
XX
PN WO200183695-A2.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013677.
XX
PR 28-APR-2000; 2000US-0200777P.
XX
PA (XIAO/) XIAO X.
XX
PI Xiao X;
XX
DR WPI; 2002-049342/06.
XX

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene.
Example 1; Page 43-44; 71pp; English.
The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta4173 containing nucleotides 1-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids)
Sequence 4182 BP; 1309 A; 927 C; 970 G; 976 T; 0 U; 0 Other;

Query Match 62.2%; Score 1245; DB 6; Length 4182;
Best Local Similarity 73.1%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 0; Indels 736; Gaps 2;
QY 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGACCGGTTATCAAACAGCTTTAGAAGAA 60
Db ||||| GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGACCGGTTATCAAACAGCTTTAGAAGAA 1059
QY 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGCAAGCACAAGGAGAGATTTCTAAT 120
Db ||||| GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGCAAGCACAAGGAGAGATTTCTAAT 1119
QY 121 GATGTGGAAGTGGTGAAGACCACTTTTCATACTCATGAGGGGTACATGATGATTTGACA 180
Db ||||| GATGTGGAAGTGGTGAAGACCACTTTTCATACTCATGAGGGGTACATGATGATTTGACA 1179
QY 181 GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATGGAACAGGA 240
Db ||||| GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATGGAACAGGA 1239
QY 241 AAATTATCAGAAGATGAAGAAACTGAAGTACAGAGCAGATGAATCTCCTAAATTCAAGA 300
Db ||||| AAATTATCAGAAGATGAAGAAACTGAAGTACAGAGCAGATGAATCTCCTAAATTCAAGA 1299
QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAGCAATTTACATAGAGTTTAAATG 360
Db ||||| TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAGCAATTTACATAGAGTTTAAATG 1359
QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAAACAAAAACAGAAAGAA 419
Db ||||| GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAAACAAAAACAGAAAGAA 1419
QY 420 ACAAGGAAAAATGGAGGAAGACCTCTTTGGACCTGATCTTGAAGACCTAAAAACGCCAAGTA 479
Db ||||| ACAAGGAAAAATGGAGGAAGACCTCTTTGGACCTGATCTTGAAGACCTAAAAACGCCAAGTA 1479
QY 480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAAACAAAGTCAGGGTCAATTCTCTC 539
Db ||||| CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAAACAAAGTCAGGGTCAATTCTCTC 1539
QY 540 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
Db ||||| ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 1599
QY 600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAACATCTGTAGATGGACAGAACACCGC 659
Db ||||| GAACAACCTTAAGGTATTGGGAGATCGATGGGCAACATCTGTAGATGGACAGAACACCGC 1659
QY 660 TGGGTTCCTTTTACAAGACATCCTTCTCAAATGGCAACGCTTTACTGAAGAACAGTGCCTT 719
Db ||||| TGGGTTCCTTTTACAAGACATCCTTCTCAAATGGCAACGCTTTACTGAAGAACAGTGCCTT 1719
QY 720 TTTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAGATTTCACACAACCTGGCTTT 779
Db ||||| TTTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAGATTTCACACAACCTGGCTTT 1779
QY 780 AAAGATCAAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTTTTTAAAAGCGGATCTA 839
Db ||||| AAAGATCAAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTTTTTAAAAGCGGATCTA 1839
QY 840 GAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 899
Db ||||| GAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 1899
QY 900 CTGAAGAATAAGTCAGTGACCCAGAAGACGGGAAGCATGGCTGGATAACTTTGCCCGGTGT 959
Db ||||| CTGAAGAATAAGTCAGTGACCCAGAAGACGGGAAGCATGGCTGGATAACTTTGCCCGGTGT 1959
QY 960 TGGGATAAATTAGTCCAAAAAACHTTGAAAAGAGTACAGCAC- - - - - 999
Db ||||| TGGGATAAATTAGTCCAAAAAACHTTGAAAAGAGTACAGCACACAGACTCATAGATTACTGCAA 2019

QY 1000 ----- 999
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QY 1000 ----- 999
Db 2080 AATGTCCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAA 2139
QY 1000 ----- 999
Db 2140 GAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTAT 2199
QY 1000 ----- 999
Db 2200 CACAACCTGGATGAAAAACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCA 2259
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Db 2260 GTCCTGTTACAAAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGA AAAAG 2319
QY 1000 ----- 999
Db 2320 TCTCTCAACATTAGTCCCATTTTGGAAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACCTT 2379
QY 1000 ----- 999
Db 2380 TCTCTGCAGGAACCTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCA 2439
QY 1000 ----- 999
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Db 2500 AGGGAATTGAAAACTAAAGAACCTGTAAATCATGAGTACTCTTGAGACTGTACGAATATTT 2559
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Db 2620 CCTGAGGAGAGAGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGAGGTCAAT 2679
QY 1000 -----AGACC 1004
Db 2680 ACTGAGTGGAAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACC 2739
QY 1005 CTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAA 1064
Db 2740 CTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAA 2799
QY 1065 GCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAA 1124
Db 2800 GCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAA 2859
QY 1125 GATCACCTCGAGAAAGTCAAGGCACCTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTG 1184
Db 2860 GATCACCTCGAGAAAGTCAAGGCACCTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTG 2919
QY 1185 AGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCAATCAGCTCTCACCGTAT 1244
Db 2920 AGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCAATCAGCTCTCACCGTAT 2979
QY 1245 AACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTTCAGGTGGCCGCTCGAG 1304
Db 2980 AACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTTCAGGTGGCCGCTCGAG 3039
QY 1305 GACCGAGTCAGGCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTT 1364
Db 3040 GACCGAGTCAGGCAGCTGCATGAAGCCACAGGGACTTTGGTCCAGCATCTCAGCACTTT 3099
QY 1365 CTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTAC 1424

Db 3100 CTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTAC 3159
QY 1425 TATATCAACCACGAGACTCAAAACAACCTTCTGGGACCATCCCAAAATGACAGAGCTCTAC 1484
Db 3160 TATATCAACCACGAGACTCAAAACAACCTTCTGGGACCATCCCAAAATGACAGAGCTCTAC 3219
QY 1485 CAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTC 1544
Db 3220 CAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTC 3279
QY 1545 CGAAGACTGCAGAAAGGCCCTTTTGGTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCC 1604
Db 3280 CGAAGACTGCAGAAAGGCCCTTTTGGTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCC 3339
QY 1605 TTGGACCAGCAACACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAAT 1664
Db 3340 TTGGACCAGCAACACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTATTAAT 3399
QY 1665 TGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCT 1724
Db 3400 TGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCT 3459
QY 1725 CTCTGCGTGGATATGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGG 1784
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Db 3520 AGGATCCGTGCTCTCTTTTAAACTGGCATCATTTCCCTGTTGTAAGCACATTTGGAA 3579
QY 1845 GACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCGC 1904
Db 3580 GACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCGC 3639
QY 1905 AGGCTGGGCTCTCTCTGCAATGATTCTATCCAAATTCRAAGACAGTTGGGTGAAGTTGCA 1964
Db 3640 AGGCTGGGCTCTCTCTGCAATGATTCTATCCAAATTCRAAGACAGTTGGGTGAAGTTGCA 3699
QY 1965 TCCTTTGGGGCAGTAACATTTGAGCCAAAGTGTCCGGA 2001
Db 3700 TCCTTTGGGGCAGTAACATTTGAGCCAAAGTGTCCGGA 3736

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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 03:01:40 ; Search time 103.19 Seconds
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Perfect score: 2001
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1002.6	50.1	5952	4	US-09-687-875A-1
2	991.6	49.6	13977	4	US-09-484-970B-60
C 3	869.8	43.5	19307	3	US-08-836-022A-10
C 4	869.8	43.5	19307	3	US-09-427-048A-10
5	490.6	24.5	6045	4	US-09-091-501B-7
6	490.6	24.5	10320	4	US-09-091-501B-9
7	460.6	23.0	3915	4	US-09-976-594-93
8	79.4	4.0	200	4	US-09-091-501B-5
9	78.6	3.9	200	4	US-09-091-501B-4
10	78.6	3.9	200	4	US-09-091-501B-6
C 11	74.6	3.7	7218	1	US-08-232-463-14
12	44.2	2.2	2574	4	US-09-668-313A-10
13	42.8	2.1	1179	4	US-09-107-532A-1186
14	42.8	2.1	1690	4	US-09-620-312D-69
15	42.8	2.1	7812	3	US-09-368-590-1
C 16	42.4	2.1	2704	3	US-08-857-076-44
C 17	42.4	2.1	3499	3	US-08-857-076-43
C 18	40.6	2.0	505	4	US-09-621-976-15639
19	39.4	2.0	832	4	US-09-621-976-2813
20	39.4	2.0	2223	1	US-08-257-073-4
C 21	39.4	2.0	193303	4	US-09-497-855A-37
C 22	39.4	2.0	193303	4	US-09-497-855A-44
23	38.8	1.9	289	3	US-09-007-005-17
24	38.8	1.9	289	3	US-09-244-796-17
25	38.8	1.9	1821	4	US-08-477-831C-1
26	38.8	1.9	1885	4	US-08-477-831C-9
27	38.8	1.9	1896	4	US-08-477-831C-10

28	38.8	1.9	1961	4	US-08-477-831C-8	Sequence 8, Appl
29	38.8	1.9	2968	4	US-08-477-831C-13	Sequence 13, Appl
30	38.8	1.9	3044	4	US-08-477-831C-12	Sequence 12, Appl
31	38.4	1.9	7672	4	US-09-220-132-24	Sequence 24, Appl
32	38.2	1.9	428	4	US-09-668-313A-3	Sequence 3, Appl
33	38.2	1.9	1848	4	US-09-134-001C-447	Sequence 447, App
34	38.2	1.9	4439	4	US-09-668-313A-17	Sequence 17, Appl
C 35	37.4	1.9	2082	3	US-08-985-335-4	Sequence 4, Appl
C 36	37.4	1.9	2082	3	US-09-410-372-4	Sequence 4, Appl
37	37.2	1.9	2160	4	US-09-092-218-1	Sequence 1, Appl
C 38	37.2	1.9	2915	4	US-09-336-115C-5	Sequence 5, Appl
C 39	37.2	1.9	3902	4	US-08-961-527-212	Sequence 212, App
40	36.8	1.8	4929	4	US-09-620-312D-674	Sequence 674, App
41	36	1.8	608	3	US-09-385-982-236	Sequence 236, App
42	36	1.8	2763	1	US-08-248-466B-2	Sequence 2, Appl
43	35.8	1.8	633	4	US-09-134-001C-578	Sequence 578, App
44	35.6	1.8	2447	2	US-09-014-969-14	Sequence 14, Appl
45	35.6	1.8	4868	1	US-08-139-937-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-687-875A-1
; Sequence 1, Application US/09687875A
; Patent No. 6544786
; GENERAL INFORMATION:
; APPLICANT: Xiao, Paul
; APPLICANT: Liu, Paul
; TITLE OF INVENTION: METHOD AND VECTOR FOR PRODUCING AND TRANSFERRING TRANS-SPLICED P
; FILE REFERENCE: 00792
; CURRENT APPLICATION NUMBER: US/09/687,875A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/158,868
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2897)..(2898)
; OTHER INFORMATION: S4 junction site
; NAME/KEY: misc feature
; LOCATION: (3198)..(3199)
; OTHER INFORMATION: S2 junction site
US-09-687-875A-1

Query Match 50.1%; Score 1002.6; DB 4; Length 5952;
Best Local Similarity 99.6%; Pred. No. 1.4e-301;
Matches 1005; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	993	ACAGCACAGACCCCTTGAAGACTCCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTC	1052
Db	3679	ATAGATGAGACCCCTTGAAGACTCCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTC	3738
QY	1053	AAGCTGCGCCCAAGCTGAGTGATCAAGGGATCCTTGGCAGCCCGTGGCGGATCTCCTCATT	1112
Db	3739	AAGCTGCGCCCAAGCTGAGTGATCAAGGGATCCTTGGCAGCCCGTGGCGGATCTCCTCATT	3798
QY	1113	GACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATTGGCGCTCTG	1172
Db	3799	GACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATTGGCGCTCTG	3858
QY	1173	AAAGAGAACGTGAGCCACGTCAATGACCTTGCTGCCAGCTTACCACCTTTGGGCATTGAG	1232
Db	3859	AAAGAGAACGTGAGCCACGTCAATGACCTTGCTGCCAGCTTACCACCTTTGGGCATTGAG	3918
QY	1233	CTCTCACCCTATAACCTCAGCACTCTGGAAGACCTGAAACACAGATGGAAGCTTCTGCAG	1292

Db 3919 CTCTCACCGTATTAACCTCAGCACTCTGGAAGACCTGAACACCCAGATGGAAGCTTCTGCGAG 3978
QY 1293 GTGGCCGTCGAGGACCGAGTCAAGGAGTGCATGAAGCCCAACAGGACTTTGGTCCAGCA 1352
Db 3979 GTGGCCGTCGAGGACCGAGTCAAGGAGTGCATGAAGCCCAACAGGACTTTGGTCCAGCA 4038
QY 1353 TCTCAGCACTTTCTTCCACGCTCTGTCAGGCTCCCTGGGAGAGAGCCATCTCGCCAAAC 1412
Db 4039 TCTCAGCACTTTCTTCCACGCTCTGTCAGGCTCCCTGGGAGAGAGCCATCTCGCCAAAC 4098
QY 1413 AAAGTGCCTTACTATATCAACCCAGAGACTCAACAACTTTGCTGGGACCATCCCAAAATG 1472
Db 4099 AAAGTGCCTTACTATATCAACCCAGAGACTCAACAACTTTGCTGGGACCATCCCAAAATG 4158
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Db 4159 ACAGAGCTCTACCACTTTTAGCTGACCTGAATAATGTGAGATTCTCAGCTTATAGACT 4218
QY 1533 GCCATGAACCTCCGAAGACTGCAGAAAGCCCTTTGCTTGGATCTCTTTGAGCCTGTGAGCT 1592
Db 4219 GCCATGAACCTCCGAAGACTGCAGAAAGCCCTTTGCTTGGATCTCTTTGAGCCTGTGAGCT 4278
QY 1593 GCATGTGATGCTTGGACCGAGCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTG 1652
Db 4279 GCATGTGATGCTTGGACCGAGCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTG 4338
QY 1653 CAGATTATTAATTGTTTGACCACTATTATGACCGCTGGAGCAAGAGCACAACAAATTG 1712
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QY 1713 GTCAACGTCCTCTCTGCTGGATATGTCTGAACCTGGCTGCTGAATGTTTATGATACG 1772
Db 4399 GTCAACGTCCTCTCTGCTGGATATGTCTGAACCTGGCTGCTGAATGTTTATGATACG 4458
QY 1773 GGACGAACAGGAGGATCCGTGTCCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAA 1832
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Db 4519 GCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATT 4578
QY 1893 TGTGACCAAGGAGGCTGGGCTCTCTGCTGATGATTTCTATCCAAATTTCCAAAGACAGTTG 1952
Db 4579 TGTGACCAAGGAGGCTGGGCTCTCTGCTGATGATTTCTATCCAAATTTCCAAAGACAGTTG 4638
QY 1953 GGTGAAGTTGCACTCTTTGGGGGCGAGTAACATTGAGCCCAAGTGTCCGGA 2001
Db 4639 GGTGAAGTTGCACTCTTTGGGGGCGAGTAACATTGAGCCCAAGTGTCCGGA 4687

RESULT 2

US-09-484-970B-60
; Sequence 60, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 60
; LENGTH: 13977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 229357.11CB1
; NAME/KEY: unsure

; LOCATION: 11721-11761, 12294, 13969
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-60
Query Match 49.6%; Score 991.6; DB 4; Length 13977;
Best Local Similarity 99.5%; Pred. No. 6.8e-298;
Matches 1005; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 993 ACAGCACAGACCCCTTGAAAGACTCCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTC 1052
Db 8993 ATAGATGAGACCCCTTGAAAGACTCCAGGAACCTTCAAGAGGCCACCGATGAGCTGGACCTC 9052
QY 1053 AAGCTGCCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCAT 1112
Db 9053 AAGCTGCCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCAT 9112
QY 1113 GACTCTCTCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCCTCTG 1172
Db 9113 GACTCTCTCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATTTGGCCTCTG 9172
QY 1173 AAAGAGAACGTGAGCCACGTCATGACCTTGTGCGCAGCTTACCACTTTGGGCAATCAG 1232
Db 9173 AAAGAGAACGTGAGCCACGTCATGACCTTGTGCGCAGCTTACCACTTTGGGCAATCAG 9232
QY 1233 CTCTCACCGTATTAACCTCAGCACTCTGGAAGACCTTGAACACAGATGGAAGCTTCTGCGAG 1292
Db 9233 CTCTCACCGTATTAACCTCAGCACTCTGGAAGACCTTGAACACAGATGGAAGCTTCTGCGAG 9292
QY 1293 GTGGCCGTCGAGGACCGAGTCAAGGAGTGCATGAAGCCCAACAGGACTTTGGTCCAGCA 1352
Db 9293 GTGGCCGTCGAGGACCGAGTCAAGGAGTGCATGAAGCCCAACAGGACTTTGGTCCAGCA 9352
QY 1353 TCTCAGCACTTTCTTCCACGCTCTGTCAGGCTCCCTGGGAGAGAGCCATCTCGCCAAAC 1412
Db 9353 TCTCAGCACTTTCTTCCACGCTCTGTCAGGCTCCCTGGGAGAGAGCCATCTCGCCAAAC 9412
QY 1413 AAAGTGCCTTACTATATCAACCCAGAGACTCAACAACTTGTGGGACCATCCCAAAATG 1472
Db 9413 AAAGTGCCTTACTATATCAACCCAGAGACTCAACAACTTGTGGGACCATCCCAAAATG 9472
QY 1473 ACAGAGCTCTACCACTTTTAGTGTGACCTGAATAATGTGAGATTCTCAGCTTATAGACT 1532
Db 9473 ACAGAGCTCTACCACTTTTAGTGTGACCTGAATAATGTGAGATTCTCAGCTTATAGACT 9532
QY 1533 GCCATGAACCTCCGAAGACTGCAGAAAGCCCTTTGCTTGGATCTCTTGGCCCTGTGAGCT 1592
Db 9533 GCCATGAACCTCCGAAGACTGCAGAAAGCCCTTTGCTTGGATCTCTTGGCCCTGTGAGCT 9592
QY 1593 GCATGTGATGCTTGGACCGAGCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTG 1652
Db 9593 GCATGTGATGCTTGGACCGAGCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTG 9652
QY 1653 CAGATTATTAATTGTTTGACCACTATTATGACCGCTGGAGCAAGAGCACAACAAATTG 1712
Db 9653 CAGATTATTAATTGTTTGACCACTATTATGACCGCTGGAGCAAGAGCACAACAAATTG 9712
QY 1713 GTCAACGTCCTCTCTGCTGGATATGTGCTGAACCTGGCTGCTGAATGTTTATGATACG 1772
Db 9713 GTCAACGTCCTCTCTGCTGGATATGTGCTGAACCTGGCTGCTGAATGTTTATGATACG 9772
QY 1773 GGACGAACAGGAGGATCCGTGTCCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAA 1832
Db 9773 GGACGAACAGGAGGATCCGTGTCCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAA 9832
QY 1833 GCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATT 1892
Db 9833 GCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATT 9892
QY 1893 TGTGACCAAGGAGGCT -GGGCTCTCTGCTGATGATTTCTATCCAAATTTCCAAAGACAGTT 1951
Db 9893 TGTGACCAAGGAGGCTGGGCTCTCTGCTGATGATTTCTATCCAAATTTCCAAAGACAGTT 9952
QY 1952 GGTGAAGTTGCACTCTTTGGGGGCGAGTAACATTGAGCCCAAGTGTCCGGA 2001

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-427-048A-10

Query Match 43.5%; Score 869.8; DB 3; Length 19307;
Best Local Similarity 91.4%; Pred. No. 8.3e-260;
Matches 922; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 993 ACAGCACAGACCCCTTGAAGACTCCAGGAACCTTCAAGAGSCACGGATGAGCTGGACCTC 1052
DB 5701 ATAGATGAAGCTCTTGAAGACTCCAGGAACCTTCAAGAGSCACGGATGAGCTGGACCTC 5642

QY 1053 AAGCTGCGCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATT 1112
DB 5641 AAGTTGCGCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCCTCATT 5582

QY 1113 GACTCTCTCAAGATCACCTCGAGAAAGTCAAGGCACCTTCAGGAGAAATTTGGGCTCTG 1172
DB 5581 GACTCTCTCAAGATCACCTTTGAAAAGTCAAGGCACCTTCGGGAGAAATTTGCACCTCTT 5522

QY 1173 AAAGAGACGTGAGCCACGTCATACCTTGTCTGCCAGCTTACCACCTTTGGGCAATTCAG 1232
DB 5521 AAAGAGATGTCAATCGTGTCAATGACCTTGCACATCAGCTGACCACACTGGGCAATTCAG 5462

QY 1233 CTCTCACCGTATAACCTCAGCCTCTGGAAGACCTTGAACACACAGATGGAAGCTTCTGCAG 1292
DB 5461 CTCTCACCTTATAACCTCAGCCTTTGGAAGATCTGAATACACAGATGGAGGCTTCTACAG 5402

QY 1293 GTGGCCGTGAGGACCGAGTCAGGAGCTGCATGAAGCCACAGGGACTTTGTGCCAGCA 1352
DB 5401 GTGGCTGTGAGGACCGGTGTCAAGACGCTGCATGAAGCCACAGGGACTTTGTCTCTGCA 5342

QY 1353 TCTCAGCACTTTCTTTCCACGCTGTCTCCAGGTCCTTGGGAGAGAGCCATCTCGCCAAAC 1412
DB 5341 TCCCAGCACTTCTTTCCACTTCAGTTCCAGGTCCTTGGGAGAGAGCCATCTCACCAAAC 5282

QY 1413 AAAGTGCCCTACTATATCAACACGAGACTCAAAACACTTGTCTGGGACCATCCCAAAATG 1472
DB 5281 AAAGTGCCCTACTATATCAACACGAGACCCAAACCACTTGTGGGACCAACCCCAAAATG 5222

QY 1473 ACAGAGCTTACCAGTCTTTAGTGCCTTGAATAATGTGATCTCTCAGCTTATAGGACT 1532
DB 5221 ACAGAGCTTACCAGTCTTTAGTGCCTTGAATAATGTGATCTCTCAGCTTATAGGACT 5162

QY 1533 GCCATGAAGCTCCGAAGACTGCAAGAGCCCTTTGCTTGGATCTCTTGGAGCCTGTGAGCT 1592
DB 5161 GCCATGAAGCTCAGAAGGCTCCGAAGGCCCCTTTGCTTGGATCTCTTGGAGCCTGTGAGCT 5102

QY 1593 GCATGTGATGCCTTGGACCCAGCACAACTTCAAGCAAAATGACCAAGCCCATGGATATCCTG 1652

DB 5101 GCATGTGATGCCCTGGACCAAGCAAACTCAAGCAAAATGACCAAGCCCATGGATATCCTG 5042
QY 1653 CAGATTATTAATTGTTTGAACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAATTTG 1712
DB 5041 CAGATAAATTAACCTGTTGACTACAAATTTATGATCGTCTGGAGCAAGAGCACAACAATCTG 4982
QY 1713 GTCAACGTCCTCTCTGCGTGGATATGTCTGAACTGGCTGTGAATGTTTATGATACG 1772
DB 4981 GTCAATGTCCTCTCTGCTGGATATGTCTCAACTGGCTTCTCAATGTTTATGATACG 4922
QY 1773 GGACGAACAGGAGGATCCGTGTCCTGCTTTTAAAACTGGCATCATTTCCCTGTGTAAA 1832
DB 4921 GGACGAACAGGAGGATCCGTGTCCTGCTTTTAAAACTGGCATCATTTCTCTGTGTAAA 4862
QY 1833 GCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTT 1892
DB 4861 GCACACTTGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACTGGCTTT 4802
QY 1893 TGTGACCAAGCAGGCTGGGCTCTCTTCTGTCATGATTTCTATCCAAATTTCCAAAGACAGTTG 1952
DB 4801 TGTGACCAAGCAGGCTGGGCTCTCTTCTGTCATGATTTCTATCCAAATTTCCAAAGACAGTTG 4742
QY 1953 GGTGAAGTTGCATCCTTTTGGGGCAGTAACATTGAGCCCAAGTGTCCGGA 2001
DB 4741 GGTGAAGTTGCTTCTTTTGGGGCAGTAACATTGAGCCCAAGTGTTCAGGA 4693

RESULT 5
US-09-091-501B-7
; Sequence 7, Application US/09091501B
; Patent No. 6518413
; GENERAL INFORMATION:
; APPLICANT: Tinsley, Jonathon M
; APPLICANT: Davies, Kay E
; TITLE OF INVENTION: Utrrophin gene expression
; FILE REFERENCE: 620-42
; CURRENT APPLICATION NUMBER: US/09/091,501B
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: PCT/GB96/03156
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: GB 9525962.8
; PRIOR FILING DATE: 1995-12-19
; PRIOR APPLICATION NUMBER: GB 9615797.9
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: GB 9622174.2
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6045
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)...(6037)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (724)...(758)
; OTHER INFORMATION: Precise residue is left open
US-09-091-501B-7

Query Match 24.5%; Score 490.6; DB 4; Length 6045;
Best Local Similarity 67.6%; Pred. No. 6.8e-142;
Matches 688; Conservative 0; Mismatches 329; Indels 0; Gaps 0;

QY 985 AAAAGAGTACAGCACAGACCCCTTGAAGACTTCCAGGAACCTTCAAGAGGCCACGATGAGC 1044
DB 3783 AAAAGCAAGTGGACAAGGCAAGGCAATTTGGAGAACTCAGAGACCTTGCAGGGAGCTATGATGACC 3842

QY 1045 TGGACCTCAAGCTGCGCCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATC 1104

Db 3843 TGGACGCTGACATGAAGAGGAGGAGAGTCCGTGCGGAATGGCTGGAAGCCCGTGGGAGACT 3902
QY 1105 TCCTCATTTGACTCTCTCCAAGATCACTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTG 1164
Db 3903 TACTCATTTGACTCGCTGCAGGATCACATTTGAAATAATCATGGCATTTAGAGAAGAAATTG 3962
QY 1165 CGCCTCTGAAAGAGAACGTTGAGCCACGTCATGACCTTGTCTGCCAGCTTACCACCTTTGG 1224
Db 3963 CACCAATCAACTTTAAAGTTAAACCGGTGAATGATTTATCCAGTCAGCTGTCTCCACTTG 4022
QY 1225 GCATTGAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAAGATGGAAGC 1284
Db 4023 ACCTGCATCCCTCTCTAAAGATGTCTCGCCAGCTAGATGACCTTAAATATGCGATGGAAC 4082
QY 1285 TTCTGCAGGTGGCGCTGAGGACCGAGTCAGGCAGCTGCATGAAGCCACAGGACTTTTG 1344
Db 4083 TTTTACAGGTTTCTGTGGATGATCGCCTTAAACAGCTTCAGGAAGCCACAGAGATTTTG 4142
QY 1345 GTCCAGCATCTCAGCACTTTCTTTCCACGTCCTGTCAGGGTCCCTGGGAGAGAGCCATCT 1404
Db 4143 GACCATCCCTCTCAGCACTTTCTCTACGTCAGTCAGCTGCCGTGGCAAAAGATCCATTT 4202
QY 1405 CGCCAAACAAAGTGCCTACTATATCAACCCAGGAGACTCAAAACAACCTGCTGGGACCATC 1464
Db 4203 CACATAATAAAGTGCCCTATTACATCAACCCATCAACACACAGACCACCTGTGGGACCATC 4262
QY 1465 CCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTGAGATTCTCAGCTT 1524
Db 4263 CTAAATGACCGCACTCTTTCAATCCCTTGTGACCTGAATAATGTACGTTTTTCTGCCT 4322
QY 1525 ATAGGACTGCCATGAAGTCCGAAGACTCGAAGACTGCAGAAGGCCCTTTTGGTCTCTTGAGCC 1584
Db 4323 ACCGTACAGCAATCAAAATCCGAAGACTACAAAAAGCACTATGTTTGGATCTCTTAGAGT 4382
QY 1585 TGTGAGCTGCATGTGATGCTCTTGGACCAAGCAACCTCAAGCAAAATGACGACCCATGG 1644
Db 4383 TGAGTACAACAAATGAATAATTTCAAACAGCAAAAGTTGAACCAAAATGACGACTCTCTCA 4442
QY 1645 ATATCCTGCAGATTATTAATGTTTGTGACCACTATTTATGACCGCTGGAGCAAGAGCACA 1704
Db 4443 GTGTTCCAGATGTATCAACTGTCTGACAACTATGATGAGCTTGACCAAAATGACATA 4502
QY 1705 ACAATTTGGTCAACGTCCCTCTCTCGGTGGATATGTGTCTGAACCTGGCTGCTGAATGTTT 1764
Db 4503 AGGACCTGGTCAACGTTCACCTCTGTGTTGATATGTGTCTCAATTTGGTTGCTCAATGTCT 4562
QY 1765 ATGATACGGGACGAACAGGAGGATCCGTGTCTCTCTTTTAAACTGGCATCATTTCCC 1824
Db 4563 ATGACACGGGTGCAACTGGAAAAAATTAGAGTGCAGAGTCTGAAGATTGGATTAATGTCTC 4622
QY 1825 TGTGTAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGCAGATTCAA 1884
Db 4623 TCTCCAAAGGTCTCTTGGAGAAAAATACAGATATCTCTTTAAGGAAGTTCGGGGCCGA 4682
QY 1885 CAGGATTTTGTGACGAGCGAGGCTGGGCTCCCTTCTGTCATGATTCTATCCAAATTCCAA 1944
Db 4683 CAGAAATGTGTGACCAAGGAGCTGGGCTGTACTTCTATGATGCCATCCAGATCCCC 4742
QY 1945 GACAGTTGGGTGAAGTTGCATCCTTTGGGGGAGTAACATTGAGCCCAAGTTCGGGA 2001
Db 4743 GGCAGCTAGGTGAAGTAGCAGCTTTTGGAGGCAAGTAATATTGAGCCTAGTGTTCGCA 4799

RESULT 6
US-09-091-501B-9
; Sequence 9, Application US/09091501B
; Patent No. 6518413
; GENERAL INFORMATION:
; APPLICANT: Tinsley, Jonathon M
; APPLICANT: Davies, Kay E
; TITLE OF INVENTION: Utrrophin gene expression
; FILE REFERENCE: 620-42
; CURRENT APPLICATION NUMBER: US/09/091,501B

; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: PCT/GB96/03156
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: GB 9525962.8
; PRIOR FILING DATE: 1995-12-19
; PRIOR APPLICATION NUMBER: GB 9615797.9
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: GB 9622174.2
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 10320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(10312)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full length
; OTHER INFORMATION: utrophin construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (724)..(758)
; OTHER INFORMATION: Precise residue is left open
US-09-091-501B-9

Query Match 24.5%; Score 490.6; DB 4; Length 10320;
Best Local Similarity 67.6%; Pred. No. 9.9e-142;
Matches 688; Conservative 0; Mismatches 329; Indels 0; Gaps 0;
QY 985 AAAAGAGTACAGCACAGACCCCTTGAAAGACTCCAGAACTTCAAGAGGCCACGGATGAGC 1044
Db 8058 AAAAGCAAGTGGACAAGGCATTGGAGAACTCAGACCTGCAGGGAGCTATGGATGACC 8117
QY 1045 TGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCCGTGGCGCATC 1104
Db 8118 TGGACGCTGACATGAAGGAGGACAGAGTCCGTGCGGAATGGCTGGAAGCCCCGTGGGAGACT 8177
QY 1105 TCCTCATTTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACCTTCGAGGAGAAATTG 1164
Db 8178 TACTCATTTGACTCGCTGCAGGATCACATTTGAAAAAATCATGGCATTTAGAGAGAAATTG 8237
QY 1165 CGCCTCTGAAAGAGAACGTTGAGCCACGTCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGG 1224
Db 8238 CACCAATCAACTTTAAAGTTAAACCGGTGAATGATTTATCCAGTCAGCTGTCTCCACTTG 8297
QY 1225 GCATTGAGCTCTCACCGTATAAACCCTCAGCACTCTGGAAGACCTGAACACCAAGATGGAAGC 1284
Db 8298 ACCTGCATCCCTCTCTAAAGATGTCTCGCCAGCTAGATGACCTTAATATGCGATGGAAC 8357
QY 1285 TTCTCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCACAGGGACTTTG 1344
Db 8358 TTTTACAGGTTTCTGTGGATGATCGCCTTAAACAGCTTCAGGAAGCCCCACAGAGATTTG 8417
QY 1345 GTCCAGCATCTCAGCACTTTTCTTCCACGTCCTGTCCAGGGTCCCTGGGAGAGAGCCATCT 1404
Db 8418 GACCATCCTCTCAGCACTTTTCTCTACGTCACTCCAGCTGCCGTGGCAAGATCCATTT 8477
QY 1405 CGCCAAACAAAGTGCCTACTATATCAACCCAGGACTCAAAACAACCTTGTCTGGGACCATC 1464
Db 8478 CACATAATAAAGTGCCCTATTACATCAACCATCAAAACACAGACCACCTGTTGGGACCATC 8537
QY 1465 CCATAATGACAGAGCTCTACAGTCTTTTAGTGACCTGAATAATGTGAGATTCTCAGCTT 1524
Db 8538 CTAAATGACCGAACTCTTTCAATCCCTTGTGACCTTGAATAATGTACGTTTTTCTGCT 8597
QY 1525 ATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCC 1584
Db 8598 ACCGTACAGCAATCAAAATCCGAAGACTACAAAAAGCACTATGTTTGGATCTCTTAGAGT 8657
QY 1585 TGTGAGCTGCATGTGATGCTTGGACCAAGCAACCTCAAGCAAAATGACCAGCCCATGG 1644


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; LENGTH: 200
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-091-501B-5

Query Match      4.0%; Score 79.4; DB 4; Length 200;
Best Local Similarity 64.3%; Pred. No. 1.1e-14;
Matches 119; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 464 CCTAAACGCCAAGTACAACAACATAAAGTGGCTTCAAGAAGATCTAGAACAAAGCAAGT 523
Db 16 CCTGCAAAACCTGCTTGAAGAACATAAAAGTTTGCAAAGTGACCTCGAAGCTGAGCAGGT 75

QY 524 CAGGGTCAATTCTCTCACTCACATGATGGTGGTAGTTGATGAATCTAGTGGAGATCACGC 583
Db 76 GAAGGTGAATTCCTTAACATCATATGTTGGTGGTGAATGATGATAAAACAGTGGGAGAGCGC 135

QY 584 AACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGCGCAAAACATCTGTAG 643
Db 136 CACAGCTGTTTGGGAAGATCAGTTACAGAAACTGGGTGAGCGCTGCACAGCTGTATGCCG 195

QY 644 ATGGA 648
Db 196 CTGGA 200
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RESULT 9
US-09-091-501B-4
; Sequence 4, Application US/09091501B
; Patent No. 6518413
; GENERAL INFORMATION:
; APPLICANT: Tinsley, Jonathon M
; APPLICANT: Davies, Kay E
; TITLE OF INVENTION: Utrrophin gene expression
; FILE REFERENCE: 620-42
; CURRENT APPLICATION NUMBER: US/09/091,501B
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: PCT/GB96/03156
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: GB 9525962.8
; PRIOR FILING DATE: 1995-12-19
; PRIOR APPLICATION NUMBER: GB 9615797.9
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: GB 9622174.2
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-091-501B-4
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Query Match      3.9%; Score 78.6; DB 4; Length 200;
Best Local Similarity 62.4%; Pred. No. 1.9e-14;
Matches 123; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 452 TGATCTTGAAGACCTAAACGCCAAGTACAACAACATAAAGTGGCTTCAAGAAGATCTAGA 511
Db 4 TGACCTGCCCTCCCTGCAGAAGCTGCTTCAAGAACATAAAAGTTTGCAAAATGACCTTGA 63

QY 512 ACAAGAACAAAGTCAGGTCAATTCTCTCACITCACATGGTGGTGGTAGTTGATGAATCTAG 571
Db 64 AGCTGAACAGGTGAAGTAAATTCCTTAACCTACATGGTGGTGAATTTGCGATGAAAACAG 123

QY 572 TGGAGATCAGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGC 631
Db 124 TGGGGAGAGTGCCACAGCTCTTCTTGGGAAGATCAGTTACAGAAACTGGGTGAGCGCTGGAC 183

QY 632 AAACATCTGTAGATGGA 648
Db 184 AGCTGTATGCCGCTGGA 200
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RESULT 10
US-09-091-501B-6
; Sequence 6, Application US/09091501B
; Patent No. 6518413
; GENERAL INFORMATION:
; APPLICANT: Tinsley, Jonathon M
; APPLICANT: Davies, Kay E
; TITLE OF INVENTION: Utrrophin gene expression
; FILE REFERENCE: 620-42
; CURRENT APPLICATION NUMBER: US/09/091,501B
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: PCT/GB96/03156
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: GB 9525962.8
; PRIOR FILING DATE: 1995-12-19
; PRIOR APPLICATION NUMBER: GB 9615797.9
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: GB 9622174.2
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-091-501B-6
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Query Match      3.9%; Score 78.6; DB 4; Length 200;
Best Local Similarity 62.4%; Pred. No. 1.9e-14;
Matches 123; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 452 TGATCTTGAAGACCTAAACGCCAAGTACAACAACATAAAGTGGCTTCAAGAAGATCTAGA 511
Db 4 TGATGTGAATCTCTACAAAAGCTGCTAGAAGAACATAAAAGTTTGCAAACTGATCTTGA 63

QY 512 ACAAGAACAAAGTCAGGTCAATTCTCTCACITCACATGGTGGTGGTAGTTGATGAATCTAG 571
Db 64 GGCTGAACACAGGTGAAAGTAAATTCACCTAACTCACATGGTGGTCAATTGTTGATGAAAACAG 123

QY 572 TGGAGATCAGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGC 631
Db 124 TGGTGAGAGCGCTACAGCTATCCTTAGAAGACCAGTTACAGAAACTTGGTGAGCGCTGGAC 183

QY 632 AAACATCTGTAGATGGA 648
Db 184 AGCAGTATGCCGTTGGA 200
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RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match
Best Local Similarity 3.7%; Score 74.6; DB 1; Length 7218;
Matches 23; Conservative 236; Mismatches 150; Indels 0; Gaps 0;

QY 113 TTCTAATGATGTGGAAGTGGTGAAGACCAAGTTTCATCTCATGAGGGTACATGATGG 172
Db 1474 TATCTATGCAAGTAGTTAAAGAGATAGAAGAAATTTGGTACRRRRRRRRRRRRRRR 1415

QY 173 ATTTGACAGCCCATCAGGCCGGTGGTAAATATTCTACAATGGGAAGTAAGTCATG 232
Db 1414 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1355

QY 233 GAACAGGAAATATATCAGAAGATGAAGAACTGAAGTACAAGACAGATGAATCTCTAA 292
Db 1354 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1295

QY 293 ATTCAAGATGGGAATGCCTCAGGGTAGCTAGCATGGAACAAACAAAGCAATTTACATAGAG 352
Db 1294 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1235

QY 353 TTTTAATGGATCTCCAGATCGAACTGAAAGAGTTGAATGACTGGCTAACAACAAACAGA 412
Db 1234 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1175

QY 413 AGAAAGAACAGGAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAACG 472
Db 1174 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1115

QY 473 CCAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGACAAGAACAA 521
Db 1114 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1066

RESULT 12
US-09-668-313A-10
; Sequence 10, Application US/09668313A
; Patent No. 6503756
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF SYNTAXIN 4 INTERACTING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0127
; CURRENT APPLICATION NUMBER: US/09/668,313A
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 247
; SEQ ID NO 10
; LENGTH: 2574

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; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (218)...(1891)
US-09-668-313A-10

Query Match
Best Local Similarity 2.2%; Score 44.2; DB 4; Length 2574;
Matches 88; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1389 TGGGAGAGAGCCCATCTCGCCAAACAAAGTGCCTTACTATATCAACACGAGACTCAAACA 1448
Db 1733 TGGGAGGAGAGCTTACACAGCAGATGGAATCAAGTACTTTCATCAACACCGTGACACAGACC 1792

QY 1449 ACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 1508
Db 1793 ACGTCTCGATCCACCCCGTGATGAGCGCCCTGAACCTGTCTGTGTCAGAGGAGAGTGAA 1852

QY 1509 GTCAGATTCTCAGCTTATAGGACTGCCCATGAAACTCCGAAG 1549
Db 1853 GAGGACTGTCCAGAGAGCTAACAGACCCGAAAGCTGATG 1893

RESULT 13
US-09-107-532A-1186
; Sequence 1186, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1179 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature

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LOCATION: (B) LOCATION 1...1179
SEQUENCE DESCRIPTION: SEQ ID NO: 1186;
US-09-107-532A-1186
Query Match 2.1%; Score 42.8; DB 4; Length 1179;
Best Local Similarity 49.5%; Pred. No. 0.0097;
Matches 110; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 353 TTTTAATGGATCCAGAAATCGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGA 412
Db 585 TGTTGATCCAGCACTTGAGCAAAAGAAATAAAGATTTGATCGATCAGACAAAGAAAAATGG 644
QY 413 AGAAGAACAAAGAAATGGAGGAAGAGCGCTCTTGGACCTGATCTTGAAGACCTAAACG 472
Db 645 AGATACGATCGAGGAATTTAGAAAGTGTCTGTTGGAGCGTTCCAGCTGGATTAGGAAG 704
QY 473 CCAAGTACAACAATAAGGTGCTTCAAGAAAGATCTAGAACAAAGAACAAAGTCAGGTCAA 532
Db 705 CTACGTACAATGGGACACGAAGCTAGATGCCAAAATCGCACAAAGCTGTGTTAGTATCAA 764
QY 533 TTCTCTCACTCAATGGTGGTGGTAGTTGATGAATCTAGTGG 574
Db 765 TGCCTTTAAAGCGTAGAATTTGGGGTCGGATTCACTTCTGG 806

RESULT 14
US-09-620-312D-69
; Sequence 69, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 69
; LENGTH: 1690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(1522)
US-09-620-312D-69

Query Match 2.1%; Score 42.8; DB 4; Length 1690;
Best Local Similarity 47.9%; Pred. No. 0.013;
Matches 156; Conservative 0; Mismatches 167; Indels 3; Gaps 1;
QY 1016 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 1075

Db 55 CAAGGAGTTGCACCAGGTGGCGCACGACCTGGACGACGAGCTGGCATGGTTTCAGGAGCG 114
QY 1076 CAAGGGA---TCCTGGCAGCCCGTGGCGGATCTCTCATTGACTCTCTCCAAGATCACCT 1132
Db 115 GCTGCCACTGGCCATGCAGACAGAGCGAGGCAACGGTTTGCAGGCGGTCCAGCAGACAT 174
QY 1133 CGAGAAAGTCAAGGCACCTTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTGAGCCACGT 1192
Db 175 CAAAAAGAACCAAGGCGCTCGCGGGAGATCCAGGCGCATGGGCGCGCTGGAGGAGGT 234
QY 1193 CAATGACCTTGCTGCCAGCTTACCACCTTTGGGCATTGAGCTCTCACCGTATAACCTCAG 1252
Db 235 GCTGAGCGCGCGCGCGCTGGCGTGGTGGCAGCCGAGGAGGAGGAGGAGGAGGAGG 294
QY 1253 CACTCTGGAAGACCTGAACACCATGATGGAAGCTTTCGAGGTGGCGCTCGAGGACCGAGT 1312
Db 295 GGGCCTGGAGCAGCTGCAGAGCGCTGGGCGGAGCTGGGAGGCTGCCGAGCGACGGCA 354
QY 1313 CAGGCAGCTGCATGAAGCCACAGGG 1338
Db 355 GCAGGTGCTGGACGCCCTTCCAGG 380

RESULT 15
US-09-368-590-1
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michelle
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
US-09-368-590-1

Query Match 2.1%; Score 42.8; DB 3; Length 7812;
Best Local Similarity 47.9%; Pred. No. 0.037;
Matches 156; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

QY 1016 CCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 1075
Db 3639 CAAGGAGTTGCACCCAGGTGGCGCACGACCTGGACGACGAGCTGGCATGGTTTCAGGAGCG 3698
QY 1076 CAAGGGA---TCCTGGCAGCCCGTGGCGGATCTCTCATTGACTCTCTCCAAGATCACCT 1132
Db 3699 GCTGCCACTGGCCATGCAGACAGAGCGGAGATCCAGGCGCATGGGCGCGCTTCAGGAGGAGT 3758
QY 1133 CGAGAAAGTCAAGGCACTTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTGAGCCACGT 1192
Db 3759 CAAAAAGAACCAAGGCGCTGGCGGGAGATCCAGGCGCATGGGCGCGCTTCAGGAGGAGT 3818
QY 1193 CAATGACCTTGCTCGCCAGCTTACCACCTTTGGGATTCAGCTCTCACCGTATAACCTCAG 1252
Db 3819 GCTGAGCGCGCGGCGGCTGGCGTGGTGGCAGCGCCGAGGAGGAGGAGGAGGAGGAGGAGG 3878

QY	1253	CACTCTGGAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGT	1312
Db	3879	GGCCTGGAGCAGCTGCAGAGCGCCTGGGCCGACTGCGGAGGCTGCCGAGCGACGGCA	3938
QY	1313	CAGGCAGCTGCATGAAGCCACAGG	1338
Db	3939	GCAGGTGCTGGACGCCGCTTCCAGG	3964

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Job time : 106.19 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 08:30:27 ; Search time 666.733 Seconds
(without alignments)
15148.395 Million cell updates/sec

Title: US-09-845-416-14_COPY_1000_3000

Perfect score: 2001

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
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- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1820.8	91.0	5417	16	US-10-149-736-39
4	1593	79.6	3510	10	US-09-845-416-12
5	1593	79.6	4476	10	US-09-845-416-31
6	1263	63.1	3858	10	US-09-845-416-9
7	1263	63.1	4825	10	US-09-845-416-29
8	1263	63.1	4848	10	US-09-845-416-35
9	1263	63.1	5060	10	US-09-845-416-36
10	1254	62.7	5339	16	US-10-149-736-40
11	1251.2	62.5	3531	10	US-09-845-416-10
12	1251.2	62.5	4498	10	US-09-845-416-30
13	1245	62.2	4182	10	US-09-845-416-2
14	1245	62.2	5149	10	US-09-845-416-27

15	1132.2	56.6	5462	16	US-10-149-736-41	Sequence 41, Appl
16	1112	55.6	3999	10	US-09-845-416-6	Sequence 6, Appli
17	1112	55.6	4966	10	US-09-845-416-28	Sequence 28, Appl
18	1112	55.6	4990	10	US-09-845-416-34	Sequence 34, Appl
19	1002.6	50.1	1821	10	US-09-845-416-13	Sequence 13, Appl
20	1002.6	50.1	2169	10	US-09-845-416-4	Sequence 4, Appli
21	1002.6	50.1	8689	16	US-10-149-736-42	Sequence 42, Appl
22	1002.6	50.1	11058	10	US-09-845-416-1	Sequence 1, Appli
23	1002.6	50.1	11443	16	US-10-149-736-44	Sequence 44, Appl
24	1002.6	50.1	12057	16	US-10-149-736-47	Sequence 47, Appl
25	1002.6	50.1	13957	9	US-09-782-378A-22	Sequence 22, Appl
26	1002.6	50.1	13957	9	US-09-880-107-2284	Sequence 2284, Ap
27	1002.6	50.1	13957	16	US-10-149-736-1	Sequence 1, Appli
28	1002.6	50.1	14069	13	US-10-342-887-434	Sequence 434, App
29	1002.6	50.1	14069	13	US-10-172-118-434	Sequence 434, App
30	1002.6	50.1	14082	13	US-10-342-887-981	Sequence 981, App
31	1002.6	50.1	14082	13	US-10-172-118-981	Sequence 981, App
32	1002.6	50.1	14082	16	US-10-341-434-108	Sequence 108, App
33	1001	50.0	1434	10	US-09-845-416-15	Sequence 15, Appl
34	985.8	49.3	1991	10	US-09-845-416-3	Sequence 3, Appli
35	869.8	43.5	13815	16	US-10-149-736-2	Sequence 2, Appli
36	665	33.2	1667	10	US-09-845-416-7	Sequence 7, Appli
37	514.6	25.7	10705	12	US-10-152-319A-1598	Sequence 1598, Ap
38	506.6	25.3	11096	16	US-10-149-736-4	Sequence 4, Appli
39	490.6	24.5	10302	9	US-09-782-378A-23	Sequence 23, Appl
40	490.6	24.5	10302	16	US-10-149-736-3	Sequence 3, Appli
41	481.8	24.1	16531	15	US-10-101-510-667	Sequence 667, App
42	470.2	23.5	5106	13	US-10-220-120-157	Sequence 157, App
43	457	22.8	887	16	US-10-149-736-35	Sequence 35, Appl
44	350	17.5	1340	10	US-09-845-416-11	Sequence 11, Appl
45	327	16.3	327	16	US-10-149-736-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-845-416-14
; Sequence 14, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 3446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-14

Query Match	100.0%;	Score	2001;	DB	10;	Length	3446;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	2001;	Conservative	0;	Mismatches	0;	Indels	0; Gaps 0;
Qy	1	GGCAGTTCATTGATGGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAGAA	60				
Db	1000	GGCAGTTCATTGATGGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAGAA	1059				
Qy	61	GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAGGAGAGATTTCTAAT	120				
Db	1060	GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAGGAGAGATTTCTAAT	1119				
Qy	121	GATGTGGAAGTGGTGAAGACCAGTTTTCATCTACTCATGAGGGGTACATGATGATTGACA	180				
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Db 1180 GCCATCAGGCGCGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAAACAGGA 1239
QY 241 AATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCTAAATTCAAGA 300
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QY 301 TGGGAATGCTCAGGGTAGCTAGATGGAAAAACAAGCAATTTACATAGAGTTTAATG 360
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QY 481 AACACATAAGGTGCTTCAAGAGATCTAGAACAAAGAACAAAGTCAGGGTCAATCTCTCA 540
Db 1480 AACACATAAGGTGCTTCAAGAGATCTAGAACAAAGAACAAAGTCAGGGTCAATCTCTCA 1539
QY 541 CTCACATGCTGGTGGTAGTTGATGAATCTAGTGGAGATCAGCAACTGCTGCTTTGGAAG 600
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QY 781 AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCGTTTTTAAAAGCGGATCTAG 840
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QY 841 AAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACAC 900
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QY 901 TGAAGATAAAGTCAGTGACCCAGAACGGAAGCATGGCTGGATAAATTTGCCCGGTGTT 960
Db 1900 TGAAGATAAAGTCAGTGACCCAGAACGGAAGCATGGCTGGATAAATTTGCCCGGTGTT 1959
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Db 2260 AAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCGTCGAGGACCGAGTCAGGCAGC 2319
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QY 1441 CTCAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACC 1500
Db 2440 CTCAAACAACTTGTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACC 2499
QY 1501 TGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGG 1560
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QY 1861 TTTTCAAGCAAGTGGCAAGTCAACAGGATTTTGTGACCAAGCGCAGGCTGGCCTCTTC 1920
Db 2860 TTTTCAAGCAAGTGGCAAGTCAACAGGATTTTGTGACCAAGCGCAGGCTGGCCTCTTC 2919
QY 1921 TGCATGATTCTATCCAAATTCOAAGACAGTTGGGTGAAGTTGCATCCCTTTGGGGCAGTA 1980
Db 2920 TGCATGATTCTATCCAAATTCOAAGACAGTTGGGTGAAGTTGCATCCCTTTGGGGCAGTA 2979
QY 1981 ACATTGAGCCCAAGTGTCCGGA 2001
Db 2980 ACATTGAGCCCAAGTGTCCGGA 3000

RESULT 2

US-09-845-416-32
; Sequence 32, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: DB1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 4414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-32

Query Match					99.5%; Score 1990; DB 10; Length 4414;				
Best Local Similarity					100.0%; Pred. No. 0;				
Matches 2001; Conservative					0; Mismatches 0; Indels 1; Gaps 1;				
QY	1	GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTTAGAAGAA	60						
Db	1757	GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTTAGAAGAA	1816						
QY	61	GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGCAAGCACACAGGAGATTTCTTAAT	120						
Db	1817	GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGCAAGCACACAGGAGATTTCTTAAT	1876						
QY	121	GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA	180						
Db	1877	GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA	1936						
QY	181	CCCCATCAGGGCCGGGTTGGTAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA	240						
Db	1937	CCCCATCAGGGCCGGGTTGGTAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA	1996						
QY	241	AAATTATCAGAAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA	300						
Db	1997	AAATTATCAGAAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA	2056						
QY	301	TGGGAATGCCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTTAATG	360						
Db	2057	TGGGAATGCCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTTAATG	2116						
QY	361	GATCTCCAGATC - GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGA	419						
Db	2117	GATCTCCAGATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGA	2176						
QY	420	ACAAAGGAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTTGAAGACCTAAAAACGCCAAGTA	479						
Db	2177	ACAAAGGAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTTGAAGACCTAAAAACGCCAAGTA	2236						
QY	480	CAACAACATAAGTGCTTCAAGAAGATCTAGAACCAAGCAAGTCAGGGTCAATTCTCTC	539						
Db	2237	CAACAACATAAGTGCTTCAAGAAGATCTAGAACCAAGCAAGTCAGGGTCAATTCTCTC	2296						
QY	540	ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA	599						
Db	2297	ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA	2356						
QY	600	GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGC	659						
Db	2357	GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGC	2416						
QY	660	TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGCTCTTACTGAAGAACAGTGCCTT	719						
Db	2417	TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGCTCTTACTGAAGAACAGTGCCTT	2476						
QY	720	TTTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAGATTCAACAACCTGGCTTT	779						
Db	2477	TTTAGTGCATGGCTTTCAGAAAAAGAGATGCAGTGAACAAGATTCAACAACCTGGCTTT	2536						
QY	780	AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTAAAAAGCGGATCTA	839						
Db	2537	AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTAAAAAGCGGATCTA	2596						
QY	840	GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA	899						
Db	2597	GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA	2656						
QY	900	CTGAAGATAAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT	959						
Db	2657	CTGAAGATAAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT	2716						
QY	960	TGGGATAATTAGTCCAAAAACTTGAAGAAGGTACAGCACAGACCCCTTGAAAGACTCCAG	1019						
Db	2717	TGGGATAATTAGTCCAAAAACTTGAAGAAGGTACAGCACAGACCCCTTGAAAGACTCCAG	2776						
QY	1020	GAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCCGCCAAGCTGAGGTGATCAAG	1079						

Db	2777	GAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCAAGCTGAGGTGATCAAG	2836						
QY	1080	GGATCCTGGCAGCCCGTGGCGGATCTCTCAATTGACTCTCTCCAAGATCACTCGAGAAA	1139						
Db	2837	GGATCCTGGCAGCCCGTGGCGGATCTCTCAATTGACTCTCTCCAAGATCACTCGAGAAA	2896						
QY	1140	GTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGTCGAGCCAGTCAATGAC	1199						
Db	2897	GTCAAGGCACCTTCGAGGAGAAATTCGCGCTCTGAAAGAGAACGTCGAGCCAGTCAATGAC	2956						
QY	1200	CTTGCTCGCCAGCTTACCACCTTTTGGGCATTGAGCTCTCACCGTATAACCTCAGCACTCTG	1259						
Db	2957	CTTGCTCGCCAGCTTACCACCTTTTGGGCATTGAGCTCTCACCGTATAACCTCAGCACTCTG	3016						
QY	1260	GAAACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG	1319						
Db	3017	GAAACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG	3076						
QY	1320	CTGCATGAAGCCCCACAGGGACCTTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTCCTGC	1379						
Db	3077	CTGCATGAAGCCCCACAGGGACCTTTTGGTCCAGCATCTCAGCACCTTTCTTCCACGTCCTGC	3136						
QY	1380	CAGGGTCCCTGGGAGAGAGCCCATCTCGCCCAACAAAGTGCCCTACTATATCAACCACGAG	1439						
Db	3137	CAGGGTCCCTGGGAGAGAGCCCATCTCGCCCAACAAAGTGCCCTACTATATCAACCACGAG	3196						
QY	1440	ACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGAC	1499						
Db	3197	ACTCAAAACAACCTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGAC	3256						
QY	1500	CTGAATAATGTGATCTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAAGACTGCAGAA	1559						
Db	3257	CTGAATAATGTGATCTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAAGACTGCAGAA	3316						
QY	1560	GCCCTTTGCTTGGATCTCTTGAGCCTGTACGTGCATGTGATGCCTTGACCGACGACAAC	1619						
Db	3317	GCCCTTTGCTTGGATCTCTTGAGCCTGTACGTGCATGTGATGCCTTGACCGACGACAAC	3376						
QY	1620	CTCAAGCAAAATGACGAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCACTATT	1679						
Db	3377	CTCAAGCAAAATGACGAGCCCATGGATATCCTGCAGATTATTAATTGTTGACCACTATT	3436						
QY	1680	TATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCTCTCTGCGTGGATATG	1739						
Db	3437	TATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCTCTCTGCGTGGATATG	3496						
QY	1740	TGCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGTGTCCTG	1799						
Db	3497	TGCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGTGTCCTG	3556						
QY	1800	TCTTTTAAAACTGSCATCATTTCCCTGTGTAAAAGCACATTTGGAAGACAAGTACAGATAC	1859						
Db	3557	TCTTTTAAAACTGSCATCATTTCCCTGTGTAAAAGCACATTTGGAAGACAAGTACAGATAC	3616						
QY	1860	CTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCGCAGGCTGGGCCTCCTT	1919						
Db	3617	CTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCGCGCAGGCTGGGCCTCCTT	3676						
QY	1920	CTGCATGATTCTATCCAAATTTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGT	1979						
Db	3677	CTGCATGATTCTATCCAAATTTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGT	3736						
QY	1980	AACATTGAGCCAAAGTGTCCCGGA	2001						
Db	3737	AACATTGAGCCAAAGTGTCCCGGA	3758						

RESULT 3
US-10-149-736-39
; Sequence 39, Application US/10149736
; Publication No. US20030216332A1
; GENERAL INFORMATION:

Db 2999 GATATCCTGCAGATTATTAAATTGTTTGACCACTATTTATGACCGCTGGAGCAAGAGCAC 3058
QY 1704 AACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGCTGAACCTGGCTGCTGAATGTT 1763
Db 3059 AACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGCTGAACCTGGCTGCTGAATGTT 3118
QY 1764 TATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAAACTGGCATCATTTCC 1823
Db 3119 TATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAAACTGGCATCATTTCC 3178
QY 1824 CTGTGTAAAGCAATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCA 1883
Db 3179 CTGTGTAAAGCAATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCA 3238
QY 1884 ACAGGATTTTGTGACCAGCGCAGGCTGGGCTCCTTCTGCAATGATTTATCCAAATTTCCA 1943
Db 3239 ACAGGATTTTGTGACCAGCGCAGGCTGGGCTCCTTCTGCAATGATTTATCCAAATTTCCA 3298
QY 1944 AGACAGTTGGGTGAAGTTGCATCCTTTTGGGGGCAGTAACATTTGAGCCAAAGTGTCCGGA 2001
Db 3299 AGACAGTTGGGTGAAGTTGCATCCTTTTGGGGGCAGTAACATTTGAGCCAAAGTGTCCGGA 3356

RESULT 4
US-09-845-416-12
; Sequence 12, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 3510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-12

Query Match 79.6%; Score 1593; DB 10; Length 3510;
Best Local Similarity 87.7%; Pred. No. 0;
Matches 1811; Conservative 0; Mismatches 190; Indels 64; Gaps 4;
QY 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTTGGACCGTTATCAAAACAGCTTTAGAAAGAA 60
Db 1000 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTTGGACCGTTATCAACAGCTTTAGAAAGAA 1059
QY 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGCAAGCACACAGGAGAGATTTCTAAT 120
Db 1060 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGCAAGCACACAGGAGAGATTTCTAAT 1119
QY 121 GATGTGGAAGTGGTGAAAGACCAGTTTTCATACTCATGAGGGGTACATGATGGATTTTGACA 180
Db 1120 GATGTGGAAGTGGTGAAAGACCAGTTTTCATACTCATGAGGGGTACATGATGGATTTTGACA 1179
QY 181 GCCCATCAGGCGCGGTTGGTAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 1180 GCCCATCAGGCGCGGTTGGTAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA 1239
QY 241 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTTCAAGA 300
Db 1240 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTTCAAGA 1299
QY 301 TGGGAATGCCTCAGGCTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTAAATG 360
Db 1300 TGGGAATGCCTCAGGCTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTAAATG 1359
QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTTGAATGACTGGCTAACAAAAACAGAAAGAA 419

Db 1360 GATCTCCAGAAATCAGAAAACCTGAAAGAGTTGTAATGACTGGCTAACAAAAACAGAAAGA 1419
QY 420 ACAAGGAAAAATGGAGGAAGAGCCTCTTTGGACCTGATCTTTGAAGACCTTAAACGCCAAGTA 479
Db 1420 ACAAGGAAAAATGGAGGAAGAGCCTCTTTGGACCTGATCTTTGAAGACCTTAAACGCCAAGTA 1479
QY 480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGCAAGTCAGGGTCAATTTCTCTC 539
Db 1480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGCAAGTCAGGGTCAATTTCTCTC 1539
QY 540 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGGCAACTGCTGCTTTGGAA 599
Db 1540 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGGCAACTGCTGCTTTGGAA 1599
QY 600 GAACAAACTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCGC 659
Db 1600 GAACAAACTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCGC 1659
QY 660 TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCCTTACTGAAGAACAGTGCCTT 719
Db 1660 TGGGTTCTTTTACAAGACAGTTCTGACCAGTGGGAAGCGTCTGCACCTTTCTCTGCAGGAA 1719
QY 720 TTTAGTGCATGGCTTTTCAGAAAAAGAAAGATGCAAGTGAACAAGATTACACAACACTGGCTTT 779
Db 1720 CTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGC 1779
QY 780 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTTAAAGCGGATCTA 839
Db 1780 GACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 1839
QY 840 GAAAAAGAAAAGCAATCCATGGGCAAACTGTA-----TTCACTCAAAACAAG 885
Db 1840 ACTAAAGAACCTGTAATCATGAGTACTCTTTGAGACTGTACGAATATTTCTGACAGAGCAG 1899
QY 886 ATCTTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAAGACGGAAGCATGGCTGGA-- 943
Db 1900 CTTTGGAAAGGACTAGAGAAAACCTCTACCAGGAGCCACAGAGCTGCCTCTCTGAGGAGAGA 1959
QY 944 -----TAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAA 978
Db 1960 GCCCAGAAATGTCACCTCGGCTTCTACGAAAGCAGCGCTGAGGAGGTCAATACTAGTGGGAA 2019
QY 979 AACTTGAA-----AAGAGTACAGCACAGACCCCTTGAAGACTC 1016
Db 2020 AAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTC 2079
QY 1017 CAGGAACTTCAAGAGCCACGGATGAGCTGAGCTGACCTCAAGCTGCGCCAAAGCTGAGGTGATC 1076
Db 2080 CAGGAACTTCAAGAGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATC 2139
QY 1077 AAGGGATCCTGGCAGCCCGTGGCGGATCTCTCATTTGACTCTCTCCTCAAGATCACCTCGAG 1136
Db 2140 AAGGGATCCTGGCAGCCCGTGGCGGATCTCTCCTCAAGATCACCTCGAG 2199
QY 1137 AAAGTCAAGGCACITTCAGAGGAGAAAATTGCGCTCTGAAAGAGAAACGTCAGGCCACGTCAT 1196
Db 2200 AAAGTCAAGGCACITTCAGAGGAGAAAATTGCGCTCTGAAAGAGAAACGTCAGGCCACGTCAT 2259
QY 1197 GACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCACT 1256
Db 2260 GACCTTGCTCGCCAGCTTACCACCTTTGGGCAATTCAGCTCTCACCGTATAACCTCAGCACT 2319
QY 1257 CTGGAAGACCTGAACACCAGATGGAAGCTTTCTGAGGTGGCCGTCGAGGACCGAGTCAGG 1316
Db 2320 CTGGAAGACCTGAACACCAGATGGAAGCTTTCTGAGGTGGCCGTCGAGGACCGAGTCAGG 2379
QY 1317 CAGCTGCATGAAGCCACAGGGACTTTTGGTCCAGCATCTCAGCACTTTTCTTTCCACGTCT 1376
Db 2380 CAGCTGCATGAAGCCACAGGGACTTTTGGTCCAGCATCTCAGCACTTTTCTTTCCACGTCT 2439
QY 1377 GTCCAGGGTCCCTGGGAGAGAGCCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCAC 1436

Db 2896 AAGGATCCTGGCAGCCCGTGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAG 2955
Qy 1137 AAAGTCAAGCAGCTTCGAGGAGAAATTCGGCCTCTGAAAGAGAACGTGAGCCACGTCAT 1196
Db 2956 AAAGTCAAGCAGCTTCGAGGAGAAATTCGGCCTCTGAAAGAGAACGTGAGCCACGTCAT 3015
Qy 1197 GACCTTGCTGGCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATACCTCAGCACT 1256
Db 3016 GACCTTGCTGGCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTATACCTCAGCACT 3075
Qy 1257 CTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGACCGAGTCAGG 1316
Db 3076 CTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGACCGAGTCAGG 3135
Qy 1317 CAGCTGCATGAAGCCCCACAGGACCTTTGGTCCAGCATCTCAGCACTTCTTTCCACGCT 1376
Db 3136 CAGCTGCATGAAGCCCCACAGGACCTTTGGTCCAGCATCTCAGCACTTCTTTCCACGCT 3195
Qy 1377 GTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCAC 1436
Db 3196 GTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCAC 3255
Qy 1437 GAGACTCAAAACAATCTGCTGGGACCATCCCAAAAATGACAGAGCTCTACCACTCTTTAGCT 1496
Db 3256 GAGACTCAAAACAATCTGCTGGGACCATCCCAAAAATGACAGAGCTCTACCACTCTTTAGCT 3315
Qy 1497 GACCTGAATAATGTCAGATTTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAG 1556
Db 3316 GACCTGAATAATGTCAGATTTCTCAGCTTATAGGACTGCCATGAACTCCGAAGACTGCAG 3375
Qy 1557 AAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTCAGCTGCATGTGATGCTTGGACCAAC 1616
Db 3376 AAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTCAGCTGCATGTGATGCTTGGACCAAC 3435
Qy 1617 AACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTTGTGACCACT 1676
Db 3436 AACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTTGTGACCACT 3495
Qy 1677 ATTTATGACCGCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCTCTCTGCGTGGAT 1736
Db 3496 ATTTATGACCGCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCTCTCTGCGTGGAT 3555
Qy 1737 ATGTGCTGAATGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTC 1796
Db 3556 ATGTGCTGAATGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTC 3615
Qy 1797 CTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGA 1856
Db 3616 CTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGA 3675
Qy 1857 TACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTGTGACCAAGCGCAGGCTGGCCCTC 1916
Db 3676 TACCTTTTCAAGCAAGTGGCAAGTTTCAACAGGATTTGTGACCAAGCGCAGGCTGGCCCTC 3735
Qy 1917 CTTCTGCATGATTCATCCAAATTCCAAGACAGTTGGGTGAAGTTGATCCTTTGGGGGC 1976
Db 3736 CTTCTGCATGATTCATCCAAATTCCAAGACAGTTGGGTGAAGTTGATCCTTTGGGGGC 3795
Qy 1977 AGTAACATTGAGCCCAAGTGTCGGGA 2001
Db 3796 AGTAACATTGAGCCCAAGTGTCGGGA 3820

RESULT 6
US-09-845-416-9
; Sequence 9, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416

; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-9

Query Match 63.1%; Score 1263; DB 10; Length 3858;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1816; Conservative 0; Mismatches 185; Indels 412; Gaps 3;

Qy 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA 60
Db 1000 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA 1059
Qy 61 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAAGGAGAGATTTCTAAT 120
Db 1060 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAAGGAGAGATTTCTAAT 1119
Qy 121 GATGTGGAAGTGGTGAAGACCAGTTTTCATACTCATGAGGGGTACATGATGGATTGACA 180
Db 1120 GATGTGGAAGTGGTGAAGACCAGTTTTCATACTCATGAGGGGTACATGATGGATTGACA 1179
Qy 181 GCCCATCAGGGCCGGTTGGTAAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 1180 GCCCATCAGGGCCGGTTGGTAAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 1239
Qy 241 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTAAATTTCAAGA 300
Db 1240 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTAAATTTCAAGA 1299
Qy 301 TGGGAATGCCTCAGGTAGCTAGCATGGAATAAATACTGGAATACTTACATAGATTTTAATG 360
Db 1300 TGGGAATGCCTCAGGTAGCTAGCATGGAATAAATACTGGAATACTTACATAGATTTTAATG 1359
Qy 361 GATCTCCAGAAATC-GAAACTGAAAGAGTTGAATGAATCTGGACCTGATCTTGAAGACCTTAAACGCAAGTA 479
Db 1360 GATCTCCAGAAATCAGAAACTGAAAGAGTTGAATGAATCTGGACCTGATCTTGAAGACCTTAAACGCAAGTA 1419
Qy 420 ACAAGGAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTTAAACGCAAGTA 479
Db 1420 ACAAGGAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTTAAACGCAAGTA 1479
Qy 480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGTCAAGTCAAGGTCATTTCTCTC 539
Db 1480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGTCAAGTCAAGGTCATTTCTCTC 1539
Qy 540 ACTCACATGGTGGTGTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
Db 1540 ACTCACATGGTGGTGTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 1599
Qy 600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCGC 659
Db 1600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCGC 1659
Qy 660 TGGGTTCTTTTACAGACACTCTTCTCAAATGSCAACGCTTACTGAAGAACAGTGCCTT 719
Db 1660 TGGGTTCTTTTACAGACACTCATAGATTACTGCAACAGTTTCCCCCTGGACCTGGAAAAG 1719
Qy 720 TTTAGTGCATGGCTTTTACAGAAAAGAGATGCACTGAACAGATTTCACACAACTGGCTTT 779
Db 1720 TTTCTTGCCTGGCTTTACAGAAAGCTGAAACAACTGCCAATGTCTCTACAGGATGCTACCCGT 1779
Qy 780 A-----AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTT 824
Db 1780 AAGGAAAGGCTCCTAGAGACTCCAAAGGGAGTAAAGAGCTGATGAACAATGGCAAGAC 1839
Qy 825 TTAAAGCGGATCTAGAAAAGAAAAGCAATCCATGGGCAAACTGTATTCTACTCAACAA 884

Db 1840 CTCCAAGGTGAATTAAGCTCACACAGATGTTTATCACAACTGGATGAAACAGCCAA 1899
QY 885 GATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGAT 944
Db 1900 AAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGAT 1959
QY 945 AACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAAATTGAAAAGAGTACAGCAC----- 999
Db 1960 AACATGAACCTCAAGTGGAGTGAACCTTCGGAATAAGTCTCTCAACATTAGTCCCATTTG 2019
QY 1000 ----- 999
Db 2020 GAAGCCAGTTCTGACCAAGTGGAAAGCTCTGCACTTTCTCTGCAGGAACCTTCTGTTGTGG 2079
QY 1000 ----- 999
Db 2080 CTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCA 2139
QY 1000 ----- 999
Db 2140 GTTCAGAAAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAAACTAAAGAACCT 2199
QY 1000 ----- 999
Db 2200 GTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCCTTTGGAAGGA 2259
QY 1000 ----- 999
Db 2260 CTAGAGAACTCTACCAGAGGCCACAGAGAGCTGCCTCTGAGGAGAGAGCCAGAAATGTC 2319
QY 1000 ----- 999
Db 2320 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTG 2379
QY 1000 -----AGACCCCTTGAAAGACTCCAGGAACTTCAA 1028
Db 2380 CACTCCGCTGACTGGCAGAGAAATAAGATGAGACCCCTTGAAAGACTCCAGGAACTTCAA 2439
QY 1029 GAGGCCAGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAAGGGATCCTGG 1088
Db 2440 GAGGCCAGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAAGGGATCCTGG 2499
QY 1089 CAGCCCGTGGCGGATCTCCTCATGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCA 1148
Db 2500 CAGCCCGTGGCGGATCTCCTCATGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCA 2559
QY 1149 CTTGAGAGAAATTTGCGCTCTGAAAGAGAAAGTCAAGTCAATGACCTTGTCTCGC 1208
Db 2560 CTTGAGAGAAATTTGCGCTCTGAAAGAGAAAGTCAAGTCAATGACCTTGTCTCGC 2619
QY 1209 CAGCTTACCACTTTGGGCATTTAGCTCTCACCCTGATAAGTCAAGTCAATGACCTTGTCTCGC 1268
Db 2620 CAGCTTACCACTTTGGGCATTTAGCTCTCACCCTGATAAGTCAAGTCAATGACCTTGTCTCGC 2679
QY 1269 AACACAGATGAAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAGGACCTGATGAA 1328
Db 2680 AACACAGATGAAAGCTTCTGAGGTGGCCGTGAGGACCGAGTCAGGACCTGATGAA 2739
QY 1329 GCCACAGGACCTTTGGTCCAGATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCCC 1388
Db 2740 GCCACAGGACCTTTGGTCCAGATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCCC 2799
QY 1389 TGGGAGAGACCATCTCGCCAAACAAAGTGCCTACTATATCAACACGAGACTCAAAACA 1448
Db 2800 TGGGAGAGACCATCTCGCCAAACAAAGTGCCTACTATATCAACACGAGACTCAAAACA 2859
QY 1449 ACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGCTTTTAGCTGACCTGAATAAT 1508
Db 2860 ACTTGTGGGACCATCCCAAAATGACAGAGCTCTACAGCTTTTAGCTGACCTGAATAAT 2919
QY 1509 GTCAGATTTCTAGGACTGACCAATGAAACTCCGAAAGACTGCAGAAAGGCCCTTTGC 1568
Db 2920 GTCAGATTTCTAGGACTGACCAATGAAACTCCGAAAGACTGCAGAAAGGCCCTTTGC 2979

QY 1569 TTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCACAACTCAAGCAA 1628
Db 2980 TTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCACAACTCAAGCAA 3039
QY 1629 AATGACCAGCCCATGGATATCTTCAGATATTAAATTTGTGACCACTATTATTATGACCGC 1688
Db 3040 AATGACCAGCCCATGGATATCTTCAGATATTAAATTTGTGACCACTATTATTATGACCGC 3099
QY 1689 CTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGCTGAAC 1748
Db 3100 CTGGAGCAAGAGCACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTGCTGAAC 3159
QY 1749 TGGCTGCTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGTGTCTCTTTTAA 1808
Db 3160 TGGCTGCTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGTGTCTCTTTTAA 3219
QY 1809 ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAGATACCTTTTCAAG 1868
Db 3220 ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAGATACCTTTTCAAG 3279
QY 1869 CAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGCCTCTCTCTGATGAT 1928
Db 3280 CAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGCCTCTCTCTGATGAT 3339
QY 1929 TCTATCCAAATTTCCAAGACAGTGGGTGAAGTTGCATCCTTTGGGGCAGTAACATTGAG 1988
Db 3340 TCTATCCAAATTTCCAAGACAGTGGGTGAAGTTGCATCCTTTGGGGCAGTAACATTGAG 3399
QY 1989 CCAAGTGTCCGGA 2001
Db 3400 CCAAGTGTCCGGA 3412

RESULT 7

US-09-845-416-29
; Sequence 29, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4825
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-29

Query Match 53.1%; Score 1263; DB 10; Length 4825;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1816; Conservative 0; Mismatches 185; Indels 412; Gaps 3;

QY 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 60
Db 1757 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 1816
QY 61 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAGGAGAGATTTCTAAT 120
Db 1817 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAGGAGAGATTTCTAAT 1876
QY 121 GATGTGGAAGTGGTGAAGACCAAGTTCATCTCATGAGGGGTACATGATGATTTGACA 180
Db 1877 GATGTGGAAGTGGTGAAGACCAAGTTCATCTCATGAGGGGTACATGATGATTTGACA 1936
QY 181 GCCCATCAGGGCCGGTTCGTAATATTCTACAATTGGGAAGTAAGCTGATGGAACAGGA 240

Db 1937 GCCCATCAGGCGGGTTGGTAATATTCTACAATTGGGAAGTAAGTGATGGAAACAGGA 1996

QY 241 AAATTATCAGAAAGATGAAGAAACTGAAGTACAAAGAGCAGATGAATCTCTAAATTCAGA 300

Db 1997 AAATTATCAGAAAGATGAAGAAACTGAAGTACAAAGAGCAGATGAATCTCTAAATTCAGA 2056

QY 301 TGGGAATGCCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTAAATG 360

Db 2057 TGGGAATGCCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTAAATG 2116

QY 361 GATCTCCAGAATC- GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGA 419

Db 2117 GATCTCCAGAATCAGAAACTGAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGA 2176

QY 420 ACAAGGAAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTAAAAACGCCAAGTA 479

Db 2177 ACAAGGAAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTAAAAACGCCAAGTA 2236

QY 480 CAACAACATAAGTGCTTCAAGAAGATCTAGAACAAAGAACAAAGTCAAGGTCATTTCTCTC 539

Db 2237 CAACAACATAAGTGCTTCAAGAAGATCTAGAACAAAGAACAAAGTCAAGGTCATTTCTCTC 2296

QY 540 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599

Db 2297 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 2356

QY 600 GAACAACTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCGC 659

Db 2357 GAACAACTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAAGACCGC 2416

QY 660 TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTT 719

Db 2417 TGGGTTCTTTTACAAGACACTCATAGATTACTGCAACAGTTCCCTCGACCTGGAAAG 2476

QY 720 TTTAGTGCATGGCTTTCAGAAAAAGAAAGCAATCCATGGCAAACTGTATTCACTCAAAACAA 779

Db 2477 TTTCTTGCTGGCTTACAGAAAGCTGAAACAACTGCCAATGTCTTACAGGATGTACCCGT 2536

QY 780 A-----AAGATCAAAATGAATGTTATCAAGTCTTCAAAAAACTGGCCGTT 824

Db 2537 AAGGAAAGGCTCCTAGAAAGACTCCAAGGGAGTAAAAAGAGCTGATGAACAAATGGCAAGAC 2596

QY 825 TTAAAAGCGGATCTAGAAAAAGAAAAAGCAATCCATGGCAAACTGTATTCACTCAAAACAA 884

Db 2597 CTCCAAGGTGAAATGAAGCTCACACAGATGTTTATCACAACTGGATGAAACACAGCCAA 2656

QY 885 GATCTTCTTTCAACACTGAAGAAATAAGTCAGTGACCCAGAAAGACGGAGCATGGCTGGAT 944

Db 2657 AAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCTCTGTTACAAAGACGTTTGGAT 2716

QY 945 AACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAAGATACAGCAC----- 999

Db 2717 AACATGAACCTTCAAGTGGAGTGAACCTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTG 2776

QY 1000 ----- 999

Db 2777 GAAGCCAGTTCTGACCAGTGAAGCGTCTGCACTTTCTCTGCAGGAACCTTCTGGTGTGG 2836

QY 1000 ----- 999

Db 2837 CTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCA 2896

QY 1000 ----- 999

Db 2897 GTTCAGAAAGCAGAACGATGTACATAGGGCTTCAAGAGGGGAATTGAAAACTAAAGAACCT 2956

QY 1000 ----- 999

Db 2957 GTAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCAGCCTTTGGAAGGA 3016

QY 1000 ----- 999

Db 3017 CTAGAGAAACTCTACCAGGAGCCACAGAGAGCTGCCTCCTGAGGAGAGAGCCACAGAATGTC 3076

QY 1000 ----- 999

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QY 1000 -----AGACCCCTTGAAAGACTCCAGGAACCTTCAA 1028

Db 3137 CACTCCGCTGACTGGCAGAGAAAAAATAGATGAGACCCCTTGAAAGACTCCAGGAACCTTCAA 3196

QY 1029 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAGGGGATCCTGG 1088

Db 3197 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAAGCTGAGGTGATCAGGGGATCCTGG 3256

QY 1089 CAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGAAAAGTCAAGGCA 1148

Db 3257 CAGCCCGTGGCGATCTCCTCATTTGACTCTCTCCAAGATCACCTCGAGAAAAGTCAAGGCA 3316

QY 1149 CTTTCAGGAGAAAAATTGCGCCTCTGAAAAGAGAACCTGAGCCACGTCAATGACCTTGCTCGC 1208

Db 3317 CTTTCGAGGAGAAAAATTGCGCCTCTGAAAAGAGAACCTGAGCCACGTCAATGACCTTGCTCGC 3376

QY 1209 CAGCTTACCACCTTTGGCAATTGAGCTCTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 1268

Db 3377 CAGCTTACCACCTTTGGSCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 3436

QY 1269 AACACCAGATGGAAGCTTCTGCAGGTGGCCGTGAGGACCGAGTCAGGCAAGTGCATGAA 1328

Db 3437 AACACCAGATGGAAGCTTCTGCAGGTGGCCGTGAGGACCGAGTCAGGCAAGTGCATGAA 3496

QY 1329 GCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCCC 1388

Db 3497 GCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCCC 3556

QY 1389 TGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAACA 1448

Db 3557 TGGGAGAGAGCCATCTCGCCAAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAACA 3616

QY 1449 ACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTTAGCTGACCTGAATAAT 1508

Db 3617 ACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTTAGCTGACCTGAATAAT 3676

QY 1509 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAAGSCCTTTTC 1568

Db 3677 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAAGSCCTTTTC 3736

QY 1569 TTGGATCTCTTGAGCCCTGCAGCTGCATGTGATGCCCTTGACCAGCACAACTCAAGCAA 1628

Db 3737 TTGGATCTCTTGAGCCCTGCAGCTGCATGTGATGCCCTTGACCAGCACAACTCAAGCAA 3796

QY 1629 AATGACCAGCCCATGGATATCTCTGCAGATTATTAATTGTTTGACCACTATTATGACCGC 1688

Db 3797 AATGACCAGCCCATGGATATCTCTGCAGATTATTAATTGTTTGACCACTATTATGACCGC 3856

QY 1689 CTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTCTCTGAAC 1748

Db 3857 CTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTCTCTGAAC 3916

QY 1749 TGCGTGTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGTGTCTGTCTTTTAAA 1808

Db 3917 TGCGTGTGAATGTTTATGATACGGGACGAAACAGGGAGGATCCGTGTCTGTCTTTTAAA 3976

QY 1809 ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAGATACCTTTTCAAG 1868

Db 3977 ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAAGTACAGATACCTTTTCAAG 4036

QY 1869 CAAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGCCCTCCTTCTGATGAT 1928

Db 4037 CAAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGCCCTCCTTCTGATGAT 4096

QY 1929 TCTATCCAAATTCCAAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCGAGTAACATTGAG 1988

Db 4097 TCTATCCAAATTCCAAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCGAGTAACATTGAG 4156

QY 1329 GCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCGTCCAGGGTCCC 1388
Db |||||
QY 3520 GCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCGTCCAGGGTCCC 3579
Db |||||
QY 1389 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCAGAGACTCAAACA 1448
Db |||||
QY 3580 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCTACTATATCAACCAGAGACTCAAACA 3639
Db |||||
QY 1449 ACTTGCTGGGACCATCCCAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 1508
Db |||||
QY 3640 ACTTGCTGGGACCATCCCAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 3699
Db |||||
QY 1509 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGC 1568
Db |||||
QY 3700 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGC 3759
Db |||||
QY 1569 TTGGATCTCTTGAGCCTGTCAGCTGCAATGTCATGCCTTTGGACCAAGCAACCTCAAGCAA 1628
Db |||||
QY 3760 TTGGATCTCTTGAGCCTGTCAGCTGCAATGTCATGCCTTTGGACCAAGCAACCTCAAGCAA 3819
Db |||||
QY 1629 AATGACCAGCCCATGGATATCCTGCAATTAATAATTGTTGACCACTATTATGACCCG 1688
Db |||||
QY 3820 AATGACCAGCCCATGGATATCCTGCAATTAATAATTGTTGACCACTATTATGACCCG 3879
Db |||||
QY 1689 CTGGAGCAAGAGACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTCTGAAC 1748
Db |||||
QY 3880 CTGGAGCAAGAGACAAATTTGGTCAACGTCCTCTCTGCGTGGATATGTCTGAAC 3939
Db |||||
QY 1749 TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGCTCTTTTAA 1808
Db |||||
QY 3940 TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGCTCTTTTAA 3999
Db |||||
QY 1809 ACTGGCATCATTTCCCTGTGTAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1868
Db |||||
QY 4000 ACTGGCATCATTTCCCTGTGTAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 4059
Db |||||
QY 1869 CAAGTGGCAAGTCAACAGGATTTTGTGACAGCGCAGGCTGGGCTCCTTCTGCAATGAT 1928
Db |||||
QY 4060 CAAGTGGCAAGTCAACAGGATTTTGTGACAGCGCAGGCTGGGCTCCTTCTGCAATGAT 4119
Db |||||
QY 1929 TCTATCCAAATTCGAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGCAGTAACATTGAG 1988
Db |||||
QY 4120 TCTATCCAAATTCGAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGCAGTAACATTGAG 4179
Db |||||
QY 1989 CCAAGTGTCGGGA 2001
Db |||||
QY 4180 CCAAGTGTCGGGA 4192
Db |||||

RESULT 9
US-09-845-416-36
; Sequence 36, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 36
; LENGTH: 5060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-36

Query Match 63.1%; Score 1263; DB 10; Length 5060;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1816; Conservative 0; Mismatches 185; Indels 412; Gaps 3;

QY 1 GGCAGTTCAATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 60
Db |||||
QY 1992 GGCAGTTCAATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 2051
Db |||||
QY 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGAAGCAACAAGGAGAGATTTCTAAT 120
Db |||||
QY 2052 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTTGAAGCAACAAGGAGAGATTTCTAAT 2111
Db |||||
QY 121 GATGTGGAAGTGGTGAAGACCAAGTTTCACTACTCATGAGGGGTACATGATGGATTTGACA 180
Db |||||
QY 2112 GATGTGGAAGTGGTGAAGACCAAGTTTCACTACTCATGAGGGGTACATGATGGATTTGACA 2171
Db |||||
QY 181 GCCCATCAGGGCCGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTTGAAACAGGA 240
Db |||||
QY 2172 GCCCATCAGGGCCGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTTGAAACAGGA 2231
Db |||||
QY 241 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTAAAATTCAAGA 300
Db |||||
QY 2232 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTAAAATTCAAGA 2291
Db |||||
QY 301 TGGGAATGCCTCAGGTFAGCTAGCATGGAAACCAAAACCAAGCAATTTACATAGAGTTTAAATG 360
Db |||||
QY 2292 TGGGAATGCCTCAGGTFAGCTAGCATGGAAACCAAAACCAAGCAATTTACATAGAGTTTAAATG 2351
Db |||||
QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAAACAAAACAGAGAAAGA 419
Db |||||
QY 2352 GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAAACAAAACAGAGAAAGA 2411
Db |||||
QY 420 ACAAGGAAAAATGGAGAGAGCCCTCTTGGACCTGATCTTGAAGACCTTAAACGCCCAAGTA 479
Db |||||
QY 2412 ACAAGGAAAAATGGAGAGAGCCCTCTTGGACCTGATCTTGAAGACCTTAAACGCCCAAGTA 2471
Db |||||
QY 480 CAACAAACATAAGGTGCTTCAAGAAGATCTAGAAACAAGACAAGTCAAGGTCAATTTCTCTC 539
Db |||||
QY 2472 CAACAAACATAAGGTGCTTCAAGAAGATCTAGAAACAAGACAAGTCAAGGTCAATTTCTCTC 2531
Db |||||
QY 540 ACTCACATGGTGGTGTGATGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
Db |||||
QY 2532 ACTCACATGGTGGTGTGATGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 2591
Db |||||
QY 600 GAACAACTTAAGGTATTTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCGC 659
Db |||||
QY 2592 GAACAACTTAAGGTATTTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCGC 2651
Db |||||
QY 660 TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCCTTACTGAAGAACAGTGCCTT 719
Db |||||
QY 2652 TGGGTTCTTTTACAAGACATCCTATAGATTTACTGCAACAGTTCCTCCCTGGACCTGGAAAAG 2711
Db |||||
QY 720 TTTAGTGCATGGCTTTACAGAAAAAAGAGATGCAGTGAACAAGATTCACACAACTGGCTTT 779
Db |||||
QY 2712 TTTCTTGCCTGGCTTACAGAAAGCTGAAACAACTGCCAATGTCTTACAGGATGTACCCGT 2771
Db |||||
QY 780 A-----AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTT 824
Db |||||
QY 2772 AAGGAAAGGCTCCTAGAGAGACTCCAAGGGAGTAAAAAGAGCTGATGAACAATGGCAAGAC 2831
Db |||||
QY 825 TTAAGGCGGATCTAGAAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAACAA 884
Db |||||
QY 2832 CTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACTGGATGAACAGCCAA 2891
Db |||||
QY 885 GATCTTCTTTCAACACTGAAGAATAAGTCAGTGAACCCAGAGACGGGAAGCATGGCTGGAT 944
Db |||||
QY 2892 AAAATCCTGAGATCCCTTGAAGGTTCCGATGATCCAGTCTCTTTACAAGACGTTTGGAT 2951
Db |||||
QY 945 AACTTTGCCCGGTGTTGGGATAATTAGTCCAAAAAATTTGAAAAGAGTACAGCAC----- 999
Db |||||
QY 2952 AACATGAACCTTCAAGTGGAGTGAACCTTCGGGAAAAAGTCTCTCAACATTTAGTCCCATTTG 3011
Db |||||
QY 1000 ----- 999
Db |||||
QY 3012 GAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACCTTTCTCTGCAGGAACCTTCTGTTGGTGG 3071
Db |||||

QY 1000 ----- 999
Db 3072 CTACAGCTGAAGATGATGAATTAAGCCGGCAGGCACCTATTTGGAGGCGACTTTCCAGCA 3131
QY 1000 ----- 999
Db 3132 GTTCAGAGCAGAACGATGTACATAGGGCCCTTCAAGAGGGAATTGAAAACCTAAAGAACCT 3191
QY 1000 ----- 999
Db 3192 GTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTTGGAAAGGA 3251
QY 1000 ----- 999
Db 3252 CTAGAGAAACTCTACAGGAGCCACAGAGAGCTGCCCTCCTGAGGAGAGAGCCCGAGAAATGTC 3311
QY 1000 ----- 999
Db 3312 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACCTAGTGGGAAAAAATTGAACCTG 3371
QY 1000 -----AGACCCCTTGAAGACTCCAGGAACCTCAA 1028
Db 3372 CACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCCTTGAAGACTCCAGGAACCTCAA 3431
QY 1029 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGATCAAGGGATCCTGG 1088
Db 3432 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAGCTGAGGTGATCAAGGGATCCTGG 3491
QY 1089 CAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGAAAGTCAAGGCA 1148
Db 3492 CAGCCCGTGGCGGATCTCCTCATTTGACTCTCTCCAAAGATCACCTCGAGAAAGTCAAGGCA 3551
QY 1149 CTTGAGGAGAAATTTGGCCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGTCTGC 1208
Db 3552 CTTGAGGAGAAATTTGGCCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGTCTGC 3611
QY 1209 CAGCTTACCACTTTGGGCATTTGAGCTCTCACCCTGATACCTCAGCACTCTGGAAGACCTG 1268
Db 3612 CAGCTTACCACTTTGGGCATTTGAGCTCTCACCCTGATACCTCAGCACTCTGGAAGACCTG 3671
QY 1269 AACACCAAGTGAAGCTTCTGACGTTGGCCGCTCGAGGACCGAGTCAGGCAGCTGCATGAA 1328
Db 3672 AACACCAAGTGAAGCTTCTGACGTTGGCCGCTCGAGGACCGAGTCAGGCAGCTGCATGAA 3731
QY 1329 GCCACAGGGACTTTGGTCCAGATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCCC 1388
Db 3732 GCCACAGGGACTTTGGTCCAGATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCCC 3791
QY 1389 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACACCGAGACTCAAACA 1448
Db 3792 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACACCGAGACTCAAACA 3851
QY 1449 ACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCACTTTTAGCTGACCTGAATAAT 1508
Db 3852 ACTTGCTGGACCATCCCAAAATGACAGAGCTCTACCACTTTTAGCTGACCTGAATAAT 3911
QY 1509 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAAGGCCCTTGC 1568
Db 3912 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAAGGCCCTTGC 3971
QY 1569 TTGGATCTCTGAGCCTGTGAGCTGCTGATGCTTGGACCGACCAACCTCAAGCAA 1628
Db 3972 TTGGATCTCTGAGCCTGTGAGCTGCTGATGCTTGGACCGACCAACCTCAAGCAA 4031
QY 1629 AATGACCAAGCCCATGGATATCCTGAGATTTAATTTGTTGACCACTATTTATGACCGC 1688
Db 4032 AATGACCAAGCCCATGGATATCCTGAGATTTAATTTGTTGACCACTATTTATGACCGC 4091
QY 1689 CTGGAGCAAGAGCACAACAATTTGGTCAACGTCCTCTGCGTGGATATGTCGTGAAC 1748
Db 4092 CTGGAGCAAGAGCACAACAATTTGGTCAACGTCCTCTGCGTGGATATGTCGTGAAC 4151
QY 1749 TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGCTCTCTTTTAA 1808

Db 4152 TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCTGTCTTTAAA 4211
QY 1809 ACTGGCATCAATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1868
Db 4212 ACTGGCATCAATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 4271
QY 1869 CAAGTGGCAAGTTCAACAGGATTTGTGACCGAGCGCAGGCTGGGCCTCCTTCTGCATGAT 1928
Db 4272 CAAGTGGCAAGTTCAACAGGATTTGTGACCGAGCGCAGGCTGGGCCTCCTTCTGCATGAT 4331
QY 1929 TCTATCCAAATTTCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCGAGTAACATTGAG 1988
Db 4332 TCTATCCAAATTTCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCGAGTAACATTGAG 4391
QY 1989 CCAAGTGTCCGGA 2001
Db 4392 CCAAGTGTCCGGA 4404

RESULT 10
US-10-149-736-40
; Sequence 40, Application US/10149736
; Publication No. US20030216332A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Harper, Scott Q.
; TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
; FILE REFERENCE: UM-06968
; CURRENT APPLICATION NUMBER: US/10/149,736
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/31126
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,848
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 5339
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-149-736-40

Query Match 62.7%; Score 1254; DB 16; Length 5339;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 380; Indels 79; Gaps 6;

QY 1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 60
Db 1199 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 1258
QY 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAGGAGAGATTCTAAT 120
Db 1259 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAGGAGAGATTCTAAT 1318
QY 121 GATGTGGAAGTGGTGAAGAACCCAGTTTCTACTACTCATGAGGGGTACATGATGGATTGACA 180
Db 1319 GATGTGGAAGTGGTGAAGAACCCAGTTTCTACTACTCATGAGGGGTACATGATGGATTGACA 1378
QY 181 GCCCATCAGGCGCGGTTGGTAAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 1379 GCCCATCAGGCGCGGTTGGTAAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 1438
QY 241 AAATTATCAGAAGATGAAGAACTGAAGTACAAAGCAGATGAATCTCCTAAATTCAAGA 300
Db 1439 AAATTATCAGAAGATGAAGAACTGAAGTACAAAGCAGATGAATCTCCTAAATTCAAGA 1498
QY 301 TGGGAATGCCCTCAGGGTAGCTAGCATGGAAAAACAAGCAATTTACATAGAGTTTAAATG 360
Db 1499 TGGGAATGCCCTCAGGGTAGCTAGCATGGAAAAACAAGCAATTTACATAGATTAATCTG 1558

QY	61	GTATTATCGTGGCTTCTTTCTGTCTGAGGACACATTGCAAGCACAAAGGAGAGATTTCTAAT	120
DB	1060	GTATTATCGTGGCTTCTTTCTGTCTGAGGACACATTGCAAGCACAAAGGAGAGATTTCTAAT	1119
QY	121	GATGTGGAAGTGGTGAAGACCAGTTTTCATACTCATGAGGGGTACATGATGGATTTGACA	180
DB	1120	GATGTGGAAGTGGTGAAGACCAGTTTTCATACTCATGAGGGGTACATGATGGATTTGACA	1179
QY	181	GCCCATCAGGGCCGGSTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA	240
DB	1180	GCCCATCAGGGCCGGSTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA	1239
QY	241	AAATTATCAGAAGATGAAGAAAACCTGAAGTACAAGACGAGATGAATCTCCTAAATTCAAGA	300
DB	1240	AAATTATCAGAAGATGAAGAAAACCTGAAGTACAAGACGAGATGAATCTCCTAAATTCAAGA	1299
QY	301	TGGGAATGCCTCAGGCTAGCTAGCATGGAAAAACAAAAGCAATTTACATAGAGTTTAAATG	360
DB	1300	TGGGAATGCCTCAGGCTAGCTAGCATGGAAAAACAAAAGCAATTTACATAGAGCTCATAGA	1359
QY	361	GATCTCCAGAA-----TCGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAA	413
DB	1360	TTACTGCAACAGTTCCCTCGACCTGGAAAAGTTTCTTGCTGGCTTACAGAAGCTGAA	1419
QY	414	GAAAGAACAAAGGAAAATGAGGAAAGAGCCTCTTGGAACCTGATCTTGAAGACCTAAAACGC	473
DB	1420	ACAACTGCCAATGTCTACAGGATGTCTACCCGTAAAGAAAGGCTCCTAGAAAGATCCCAAG	1479
QY	474	CAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGAAACAAGAACAAAGTCAGGTCAAAT	533
DB	1480	GGAGTAAAAGAGCTGATGAACAAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACA	1539
QY	534	TCTCTCACTCACATGGTGGTGGTAGTTGATGA-----ATCTAGTGGAGATCAC	581
DB	1540	GATGTTTATCACAACTGGATGAAAACAGCCAAAAAATCTGAGATCCCTGGAAGGTTC	1599
QY	582	GCAACTGCTGCTTTTGGAAACAACCTTAAGG---TATTGGGAGATCGATGGGCAAAACATC	638
DB	1600	GATGATGCAGTCTCTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACCTT	1659
QY	639	TGTAGATGGACAGAACCGCTGGGTTCTTTTACAAAGACATCCTTCTCAAATGCGAACCGT	698
DB	1660	CGGAAAAGTCTCTCAACATTAGGTCCCATTTTGGAAAGCCAGTTCTGACCAGTGGAAAGCGT	1719
QY	699	CTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGAAAAAGAAAGATGCACGTGAAC	758
DB	1720	CTGCACCTTTCTCTGCAGGAACCTTCTGGTGGCTACAGCTGAAAGATGATGAATTAAAGC	1779
QY	759	AAGATTACACAACACTGCTTTTAAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTG	818
DB	1780	CGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAAGCAGAACGATGTACATAGG	1839
QY	819	GCCGTTTTAAAGCGGATCTAGAAAAGAAAAAGCAATCCATGGGCAAACTGTA-----	871
DB	1840	GCCTTCAAGAGGGAAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTA	1899
QY	872	-----TTCACTCAAAACAAGATCTTCTTTTCAACACTGAAGAATAAGTCAGTGAACCCAGA	924
DB	1900	CGAATATTTCTGACAGAGCCAGCCTTTTGGAAGGACTAGAGAAACTCTACCAGGAGGCCAGA	1959
QY	925	AGACGGAAGCATGGCTGGA-----TAACTTTGCCCGGT	957
DB	1960	GAGCTGCCTCCTGAGGAGAGAGGCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAG	2019
QY	958	GTTGGGATAATTTAGTCCAAAAAATTGAA-----AAGAGTACA	995
DB	2020	GAGGTCAATACTGAGTGGGAAAAAATTGAACTTGCATCTCGCTGACTGGCAGAGAAAAATA	2079
QY	996	GCAACAGACCTTTGAAAGACTCCAGGAACCTTCAAGAGGCCACCGGATGAGCTGGACCTCAAG	1055
DB	2080	GATGAGACCTTTGAAAGACTCCAGGAACCTTCAAGAGGCCACCGGATGAGCTGGACCTCAAG	2139
QY	1056	CTGCGCCAAAGCTGAGGTGATCAAGGGATCTTGGCAGCCCGTGGCGGATCTCCTCATTTGAC	1115

Db	2140	CTGCGCCAAAGCTCAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCTCTCATTTGAC	2199
QY	1116	TCTCTCCAAGATCACCTCGAGAAAAGTCAAGGCACCTTCGAGGAGAAAATTGCGCTCTGAAA	1175
Db	2200	TCTCTCCAAGATCACCTCGAGAAAAGTCAAGGCACCTTCGAGGAGAAAATTGCGCTCTGAAA	2259
QY	1176	GAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTTACCACTTTGGGCATTCAGCTC	1235
Db	2260	GAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTTACCACTTTGGGCATTCAGCTC	2319
QY	1236	TCACCGTATAACCTCAGCACCTCTGGAAGACCTTGAACACCAGATGGAAGCTTCTGCAGGTG	1295
Db	2320	TCACCGTATAACCTCAGCACCTCTGGAAGACCTTGAACACCAGATGGAAGCTTCTGCAGGTG	2379
QY	1296	GCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCAACAGGGACCTTTGGTCCAGCATCT	1355
Db	2380	GCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCAACAGGGACCTTTGGTCCAGCATCT	2439
QY	1356	CAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAA	1415
Db	2440	CAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAA	2499
QY	1416	GTGCCCTACTATATCAACCACGAGACTCAAAACAATTGCTGGGACCATCCCCAAAATGACA	1475
Db	2500	GTGCCCTACTATATCAACCACGAGACTCAAAACAATTGCTGGGACCATCCCCAAAATGACA	2559
QY	1476	GAGCTCTACCAAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCC	1535
Db	2560	GAGCTCTACCAAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCC	2619
QY	1536	ATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTACAGCTGCA	1595
Db	2620	ATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTACAGCTGCA	2679
QY	1596	TGTGATGCCCTTGACCAAGCACAACTCAAGCAAAAATGACCAAGCCCATGGATATCCTGCAG	1655
Db	2680	TGTGATGCCCTTGACCAAGCACAACTCAAGCAAAAATGACCAAGCCCATGGATATCCTGCAG	2739
QY	1656	ATTATTAATTGTTGACCACTATTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTC	1715
Db	2740	ATTATTAATTGTTGACCACTATTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTC	2799
QY	1716	AACGTCCCTCTCTCGTGGATATGTGTCTGAATGGCTGCTGAATGTTTATGATACGGGA	1775
Db	2800	AACGTCCCTCTCTCGTGGATATGTGTCTGAATGGCTGCTGAATGTTTATGATACGGGA	2859
QY	1776	CGAACAGGGAGGATCCGTGTCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA	1835
Db	2860	CGAACAGGGAGGATCCGTGTCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA	2919
QY	1836	CATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCACACGGAATTTGT	1895
Db	2920	CATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCACACGGAATTTGT	2979
QY	1896	GACCAGCGCAGGCTGGGCCCTCCTTCTGCAATGATTTCTATCCAAATTCCAAGACAGTTGGGT	1955
Db	2980	GACCAGCGCAGGCTGGGCCCTCCTTCTGCAATGATTTCTATCCAAATTCCAAGACAGTTGGGT	3039
QY	1956	GAAGTTGCATCCTTTGGGGCGAGTAACATTGAGCCAAAGTGTCCCGGA	2001
Db	3040	GAAGTTGCATCCTTTGGGGCGAGTAACATTGAGCCAAAGTGTCCCGGA	3085

RESULT 12
US-09-845-416-30
; Sequence 30, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142

; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-30

Query Match 62.5%; Score 1251.2; DB 10; Length 4498;
Best Local Similarity 77.8%; Pred. No. 0;
Matches 1623; Conservative 0; Mismatches 378; Indels 85; Gaps 6;

QY 1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 60
Db 1757 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 1816

QY 61 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACACAGGAGAGATTTCTAAT 120
Db 1817 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACACAGGAGAGATTTCTAAT 1876

QY 121 GATGTGGAAGTGGTGAAAGACCAGTTCATCTACTACTCATGAGGGGTACATGATGGATTTGACA 180
Db 1877 GATGTGGAAGTGGTGAAAGACCAGTTCATCTACTCATGAGGGGTACATGATGGATTTGACA 1936

QY 181 GCCCATCAGGGCCGGGTTGGTAATATTCTACAAATTTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 1937 GCCCATCAGGGCCGGGTTGGTAATATTCTACAAATTTGGGAAGTAAGCTGATTGGAACAGGA 1996

QY 241 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTCTAAATTCAAAGA 300
Db 1997 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTCTAAATTCAAAGA 2056

QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTAAATG 360
Db 2057 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAACTCATAGA 2116

QY 361 GATCTCCAGAA-----TCGAAACTGAAGAGTTGAATGACTGGCTAAACAAAAACAGAA 413
Db 2117 TTAAGTCAACAGTTCCCTGGACCTGGAAAAAGTTTCTTGCTGGCTTACAGAAGCTGAA 2176

QY 414 GAAAGAACAAAGGAAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTTAAACGC 473
Db 2177 ACAACTGCCAATGTCTACAGGATGCTACCCGTAAAGGAAAGGCTCTAGAAGACTCCAAG 2236

QY 474 CAAGTACAACAACATAAAGGTGCTTCAAGAAGATCTAGAACAAAGAACAAAGTCAAGGTCAAT 533
Db 2237 GGAGTAAAGAGTGATGAACAATGGCAAGACCTCCAAGGTGAATTTGAAGTCAACACA 2296

QY 534 TCTCTCACTCACATGGTGGTGGTAGTTGTGA-----ATCTAGTGGAGATCAC 581
Db 2297 GATGTTTATCACACACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGGTTCC 2356

QY 582 GCAACTGCTGCTTGGAGAACAACTTAAG---TATTGGGAGATCGATGGGCAACATC 638
Db 2357 GATGATGCAGTCTCTTACAAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACIT 2416

QY 639 TGTAGATGGACAGAGACCGCTGGGTTCTTTTACAAGACATCCCTTCTCAAAATGGCAACGT 698
Db 2417 CGGAAAAAGTCTCTCAACATTAGGTCCCAATTTGGAAGCCAGTTCTGACCAGTGGAAAGCGT 2476

QY 699 CTTACTGAAGAACAGTGCCTTTTGTAGTGAATGGCTTTTCAGAAAAAGAAAGATGCAGTGAAC 758
Db 2477 CTGCACCTTTCTCTGCAGGAACCTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGC 2536

QY 759 AAGATTACACAACTGGCTTTTAAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTG 818
Db 2537 CGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTTCAGAAGCAGAACGATGTACATAGG 2596

QY 819 GCCGTTTTTAAAGCGGATCTAGAAAAAGAAAAAGCAATCCATGGGCAAACTGTA----- 871

Db 2597 GCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAAATCATGATGACTCTTGTAGACTGTA 2656
QY 872 -----TTCACTCAAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTACCCAG 924
Db 2657 CGAATATTCTGACAGACAGCCCTTTGGAGGAGGACTAGAGAACTCTACCAAGGAGCCAG 2716
QY 925 AGACGGAAGCATGGCTGGA-----TAACTTTGGCCCGGT 957
Db 2717 GAGCTGCCTCTGTGAGGAGAGAGCCAGAAATGTCACTGGCTTCTACGAAACGAGGCTGAG 2776
QY 958 GTTGGGATAATTAGTCCAAAAACTTGAA-----AAGAGTACA 995
Db 2777 GAGGTCAATACTGAGTGGGAAAAAATTGAACCTGCACCTCCGTGACTGGCAGAGAAAAATA 2836
QY 996 GCACAGACCCCTTGAAGAACTCCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAG 1055
Db 2837 GATGAGACCCCTTGAAGAACTCCAGGAACCTTCAAGAGGCCACGGATGAGCTGGACCTCAAG 2896
QY 1056 CTGCGCCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTGAC 1115
Db 2897 CTGCGCCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTGAC 2956
QY 1116 TCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAAAATTGGCGCTCTGAAA 1175
Db 2957 TCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAAAATTGGCGCTCTGAAA 3016
QY 1176 GAGAACGTGAGCCACGTCAATGACCTTGCTCGCAGCTTACCACCTTTGGGCATTGAGCTC 1235
Db 3017 GAGAACGTGAGCCACGTCAATGACCTTGCTCGCAGCTTACCACCTTTGGGCATTGAGCTC 3076
QY 1236 TCACCGTATAACCTCAGCACTCTGGAAGACCTGAAACACACAGATGGAAGCTTCTGCAGGTG 1295
Db 3077 TCACCGTATAACCTCAGCACTCTGGAAGACCTGAAACACACAGATGGAAGCTTCTGCAGGTG 3136
QY 1296 GCCGTGAGGACCGGAGTCAGGCAGCTGCATGAAGCCACACAGGAGCTTTGGTCCAGCATCT 1355
Db 3137 GCCGTGAGGACCGGAGTCAGGCAGCTGCATGAAGCCACACAGGAGCTTTGGTCCAGCATCT 3196
QY 1356 CAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAA 1415
Db 3197 CAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAA 3256
QY 1416 GTGCCCTACTATATCAACACGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACA 1475
Db 3257 GTGCCCTACTATATCAACACGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACA 3316
QY 1476 GAGCTCTACAGTCTTTAGCTGACCTGAATAATGTGATGATTTCTAGCTTATAGGACTGCC 1535
Db 3317 GAGCTCTACAGTCTTTAGCTGACCTGAATAATGTGATGATTTCTAGCTTATAGGACTGCC 3376
QY 1536 ATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCA 1595
Db 3377 ATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCA 3436
QY 1596 TGTGATGCCCTTGGACAGCACAAACCTCAAGCAAAAATGACCAGCCCATGGATATCCTGCAG 1655
Db 3437 TGTGATGCCCTTGGACAGCACAAACCTCAAGCAAAAATGACCAGCCCATGGATATCCTGCAG 3496
QY 1656 ATTATTAATTGTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTC 1715
Db 3497 ATTATTAATTGTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTC 3556
QY 1716 AACGTCCCTCTCTGCGTGGATATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGA 1775
Db 3557 AACGTCCCTCTCTGCGTGGATATGTGTCTGAACCTGGCTGCTGAATGTTTATGATACGGGA 3616
QY 1776 CGAACAGGGAGGATCCGTGCTCTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA 1835
Db 3617 CGAACAGGGAGGATCCGTGCTCTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA 3676
QY 1836 CATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGT 1895

Db 3677 CATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGT 3736
QY 1896 GACCAGCGCAGGCTGGCCCTCCTTCTGTCATGATTTCTATCCAAATTCGAAGACAGTTGGGT 1955
Db 3737 GACCAGCGCAGGCTGGCCCTCCTTCTGTCATGATTTCTATCCAAATTCGAAGACAGTTGGGT 3796
QY 1956 GAAGTTGCATCCTTTTGGGGGCGAGTAACATTGAGCCCAAGTGTCCGGA 2001
Db 3797 GAAGTTGCATCCTTTTGGGGGCGAGTAACATTGAGCCCAAGTGTCCGGA 3842

RESULT 13
US-09-845-416-2
; Sequence 2, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-2

Query Match 62.2%; Score 1245; DB 10; Length 4182;
Best Local Similarity 73.1%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 0; Indels 736; Gaps 2;

QY 1 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA 60
Db 1000 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA 1059
QY 61 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTAAT 120
Db 1060 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAAGGAGAGATTCTAAT 1119
QY 121 GATGTGGAAGTGGTGAAGAACCCAGTTTCATACTCATGAGGGGTACATGATGGATTGACA 180
Db 1120 GATGTGGAAGTGGTGAAGAACCCAGTTTCATACTCATGAGGGGTACATGATGGATTGACA 1179
QY 181 GCCCATCAGGCGCGGTTGGTAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 1180 GCCCATCAGGCGCGGTTGGTAATATTCTACAAATTGGGAAGTAAGCTGATTGGAACAGGA 1239
QY 241 AAATTATCAGAAGATGAAGAACTGAAGTACAAAGACAGCATGAATCTCCTAAATTCAAGA 300
Db 1240 AAATTATCAGAAGATGAAGAACTGAAGTACAAAGACAGCATGAATCTCCTAAATTCAAGA 1299
QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTAATG 360
Db 1300 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTAATG 1359
QY 361 GATCTCCAGAATC-GAAACTGAAGAGTTGAATGACTGGCTAACAAAAACAGAAAGAA 419
Db 1360 GATCTCCAGAATCAGAATCAGAATCAGAAGAGTTGAATGACTGGCTAACAAAAACAGAAAGAA 1419
QY 420 ACAAGGAAATGGAGGAAGAGCCCTTTGGACCTGATCTTGAAGACCTTAAACGCCAAGTA 479
Db 1420 ACAAGGAAATGGAGGAAGAGCCCTTTGGACCTGATCTTGAAGACCTTAAACGCCAAGTA 1479
QY 480 CAACAACATAAGGTGCTTCAAGAGATCTAGAACAAAGAACAAAGTCAAGGTCAATCTCTC 539
Db 1480 CAACAACATAAGGTGCTTCAAGAGATCTAGAACAAAGAACAAAGTCAAGGTCAATCTCTC 1539
QY 540 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599

Db 1540 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 1599
QY 600 GAACAACCTTAAGGTATTGGGAGATCGATGGCAAAACATCTGTAGATGGACAGAACCCGC 659
Db 1600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCGC 1659
QY 660 TGGGTCTTTTACAAGACATCCTTCTCAAATGGCAACGCTTCTTACTGAAGAACAGTGCCTT 719
Db 1660 TGGGTCTTTTACAAGACATCCTTCTCAAATGGCAACGCTTCTTACTGAAGAACAGTGCCTT 1719
QY 720 TTTAGTGCATGGCTTTTCAGAAAAAGAAAGATGCAGTGAACAAGATTTCACACAACCTGGCTTT 779
Db 1720 TTTAGTGCATGGCTTTTCAGAAAAAGAAAGATGCAGTGAACAAGATTTCACACAACCTGGCTTT 1779
QY 780 AAAGATCAAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTTTTTAAAGCGGATCTA 839
Db 1780 AAAGATCAAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCCGTTTTTAAAGCGGATCTA 1839
QY 840 GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 899
Db 1840 GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 1899
QY 900 CTGAAGAATAAGTCAGTGACCCAGAAAGACGGAAAGCATGGCTGGATAAATTTGCCCGGTGT 959
Db 1900 CTGAAGAATAAGTCAGTGACCCAGAAAGACGGAAAGCATGGCTGGATAAATTTGCCCGGTGT 1959
QY 960 TGGGATAAATTTAGTCCAAAAACTTGAAAAAGAGTACAGCAC----- 999
Db 1960 TGGGATAAATTTAGTCCAAAAACTTGAAAAAGAGTACAGCACAGACTCATAGATTACTGCAA 2019
QY 1000----- 999
Db 2020 CAGTTCCCTCCCTGGACCTGGAAAAAGTTTCTTGCCTGGCTTACAGAAGCTGAAAAACAAGTCC 2079
QY 1000----- 999
Db 2080 AATGTCCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGAGTAAAA 2139
QY 1000----- 999
Db 2140 GAGCTGATGAAACAATGGCAAGACCTCCAAAGGTGAATTTGAAGCTCACACAGATGTTTAT 2199
QY 1000----- 999
Db 2200 CACAACCTGGATGAAAAACAGCCAAAAAATCCTGAGATCCCTGGAAAGTTCCGATGATGCA 2259
QY 1000----- 999
Db 2260 GTCCTGTACAAGACGTTTGGATAAATGAACCTTCAAGTGGAGTGAACTTCGGAAAAAAG 2319
QY 1000----- 999
Db 2320 TCTCTCAACATTAGGTCCCAATTTGGAAGCCAGTTCTGACCAGTGGAAAGCGTCTGCACCTT 2379
QY 1000----- 999
Db 2380 TCTCTGAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCA 2439
QY 1000----- 999
Db 2440 CCTATTGGAGGCGACTTTCCAGCAGTTTCAAGAGCAGAACGATGTACATAGGGCCTTCAAG 2499
QY 1000----- 999
Db 2500 AGGGAATTGAAAACTAAAGAACTGTAATCATGAGTACTTTGAGACTGTACGAATATTT 2559
QY 1000----- 999
Db 2560 CTGACAGAGCAGCCTTTTGGAAAGACTAGAGAACTCTACCAGGAGCCAGAGAGCTGCCT 2619
QY 1000----- 999

Db 2620 CCTGAGGAGAGCCCCAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGTCAAT 2679
QY 1000 -----AGACC 1004
Db 2680 ACTGAGTGGGAAAAATTGAACCTGCACCTCCGCTGACTGGCAGAGAAAAATAGATGAGACC 2739
QY 1005 CTTGAAAGACTCCAGGAACCTTCAAGAGAGCCACGGATGAGCTGGACCTCAAGCTGGCCCAA 1064
Db 2740 CTTGAAAGACTCCAGGAACCTTCAAGAGAGCCACGGATGAGCTGGACCTCAAGCTGGCCCAA 2799
QY 1065 GCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCTCTCAATTGACTCTCTCCAA 1124
Db 2800 GCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGCGGATCTCTCTCAATTGACTCTCTCCAA 2859
QY 1125 GATCACCTCGAGAAAGTCAAGGCATCTTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTG 1184
Db 2860 GATCACCTCGAGAAAGTCAAGGCATCTTCGAGGAGAAATTGGCCCTCTGAAAGAGAACGTG 2919
QY 1185 AGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTAT 1244
Db 2920 AGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTAT 2979
QY 1245 AACCTCAGCACTCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTCGAG 1304
Db 2980 AACCTCAGCACTCTGGAAGACCTGAACACACAGATGGAAGCTTCTGAGGTGGCCGTCGAG 3039
QY 1305 GACCGAGTCAGGCGAGCTGCATGAAGCCCAAGGGACCTTTGGTCCAGCATCTCAGCACTTT 1364
Db 3040 GACCGAGTCAGGCGAGCTGCATGAAGCCCAAGGGACCTTTGGTCCAGCATCTCAGCACTTT 3099
QY 1365 CTTTCCACGTCTGCCAGGTCCTCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTAC 1424
Db 3100 CTTTCCACGTCTGCCAGGTCCTCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTAC 3159
QY 1425 TATATCAACCACGAGACTCAACAACTTGTGGGACCATCCCCAAATGACAGACTCTAC 1484
Db 3160 TATATCAACCACGAGACTCAACAACTTGTGGGACCATCCCCAAATGACAGACTCTAC 3219
QY 1485 CAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTC 1544
Db 3220 CAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACTC 3279
QY 1545 CGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTCAGTGCATGTGATGCC 1604
Db 3280 CGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCCTGTCAGTGCATGTGATGCC 3339
QY 1605 TTGGACCAAGCAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAAAT 1664
Db 3340 TTGGACCAAGCAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAAAT 3399
QY 1665 TGTTTGACCACTATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCT 1724
Db 3400 TGTTTGACCACTATTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCT 3459
QY 1725 CTCTGCGTGGATATGTGTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGG 1784
Db 3460 CTCTGCGTGGATATGTGTGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGG 3519
QY 1785 AGGATCCGTGTCCTGTCTTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTTGAA 1844
Db 3520 AGGATCCGTGTCCTGTCTTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTTGAA 3579
QY 1845 GACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAAGCCG 1904
Db 3580 GACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAAGCCG 3639
QY 1905 AGGCTGGGCCTCCTCTCTGCATGATTCTATCCAAATTCGAAGACAGTTGGGTGAAGTTGCA 1964
Db 3640 AGGCTGGGCCTCCTCTCTGCATGATTCTATCCAAATTCGAAGACAGTTGGGTGAAGTTGCA 3699
QY 1965 TCCTTTGGGGGCAGTAACATTGAGCCCAAGTTCGGGA 2001
Db 3700 TCCTTTGGGGGCAGTAACATTGAGCCCAAGTTCGGGA 3736

RESULT 14

US-09-845-416-27
; Sequence 27, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; FILE REFERENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 5149
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-416-27

Query Match 62.2%; Score 1245; DB 10; Length 5149;

Best Local Similarity 73.1%; Pred. No. 0;

Matches 2001; Conservative 0; Mismatches 0; Indels 736; Gaps 2;

QY 1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA 60
Db 1757 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAAGAA 1816
QY 61 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAAAGGAGAGATTTCTAAT 120
Db 1817 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAAAGGAGAGATTTCTAAT 1876
QY 121 GATGTGGAAGTGGTGAAGACCAAGTTCATCTACTCATGAGGGGTACATGATGGATTTGACA 180
Db 1877 GATGTGGAAGTGGTGAAGACCAAGTTCATCTACTCATGAGGGGTACATGATGGATTTGACA 1936
QY 181 GCCCATCAGGCCGGTGGTAAATATTCATAATTTGGGAAGTAAGCTGATGGAAACAGGA 240
Db 1937 GCCCATCAGGCCGGTGGTAAATATTCATAATTTGGGAAGTAAGCTGATGGAAACAGGA 1996
QY 241 AAATTATCAGAAGATGAAGAAAACCTGAAGTACAAGAGCAGATGAATCTCTAAATTTCAAGA 300
Db 1997 AAATTATCAGAAGATGAAGAAAACCTGAAGTACAAGAGCAGATGAATCTCTAAATTTCAAGA 2056
QY 301 TGGGAATGCCTCAGGTPAGCTAGCATGGAAAACCTGAAGTGAATGACTGGCTAACAAAAACAGAGAAAGA 419
Db 2057 TGGGAATGCCTCAGGTPAGCTAGCATGGAAAACCTGAAGTGAATGACTGGCTAACAAAAACAGAGAAAGA 2116
QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAGAAAGA 419
Db 2117 GATCTCCAGAATCAGAAAACCTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAGAAAGA 2176
QY 420 ACAAGGAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTTGAAGACCTTAAACGCCCAAGTA 479
Db 2177 ACAAGGAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTTGAAGACCTTAAACGCCCAAGTA 2236
QY 480 CAACAACATAAGGTGCTTCAAGAAAGATCTAGAACAAAGACAAGTCAAGGTCAATTCTCTC 539
Db 2237 CAACAACATAAGGTGCTTCAAGAAAGATCTAGAACAAAGACAAGTCAAGGTCAATTCTCTC 2296
QY 540 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
Db 2297 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 2356
QY 600 GAACAACTTAAGGTATTTGGGAGATCGATGGGCAACATCTGTAGATGGACAGAACCCGC 659
Db 2357 GAACAACTTAAGGTATTTGGGAGATCGATGGGCAACATCTGTAGATGGACAGAACCCGC 2416
QY 660 TGGGTTCTTTTACAGACATCTCTCAAATGGCAACGCTCTTACTGAAGAACAGTGCCTT 719

Db 2417 TGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGCTTACTGAAGAACAGTGCCTT 2476
QY 720 TTTAGTGCATGGCTTTTACAGAAAAAGAGATGCAGTGAACAGATTCACACAACTGGCTTT 779
Db 2477 TTTAGTGCATGGCTTTTACAGAAAAAGAGATGCAGTGAACAGATTCACACAACTGGCTTT 2536
QY 780 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGCCGTTTTTAAAGCGGATCTA 839
Db 2537 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGCCGTTTTTAAAGCGGATCTA 2596
QY 840 GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 899
Db 2597 GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 2656
QY 900 CTGAAGATAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT 959
Db 2657 CTGAAGATAAGTCAGTGACCCAGAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT 2716
QY 960 TGGGATAATTAGTCCAAAAAATTGAAAAAGAGTACAGCAC 999
Db 2717 TGGGATAATTAGTCCAAAAAATTGAAAAAGAGTACAGCACAGACTCATAGATTACTGCAA 2776
QY 1000 ----- 999
Db 2777 CAGTTCCCCCTGGACCTGGAAAAAGTTTCTTGCTGGCTTACAGAAGCTGAAACAAGTGC 2836
QY 1000 ----- 999
Db 2837 AATGTCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGAGTAAAA 2896
QY 1000 ----- 999
Db 2897 GAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTAT 2956
QY 1000 ----- 999
Db 2957 CACAACCTGSATGAAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGTTCCGATGATGCA 3016
QY 1000 ----- 999
Db 3017 GTCCTGTTACAAAGACGTTTGGGATAACATGAACCTTCAAGTGGAGTGAACCTTCGGAANAAG 3076
QY 1000 ----- 999
Db 3077 TCTCTCAACATTAGTCCCATTTTGAAGCCAGTTCTGACCAGTGGAGCGTCTGCACCTT 3136
QY 1000 ----- 999
Db 3137 TCTCTGCAGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGCGCAGGCA 3196
QY 1000 ----- 999
Db 3197 CCTATTGAGGCGGACTTTCCAGCAGTTCCAGAGCAGAACGATGATAGGGCCTTCAAG 3256
QY 1000 ----- 999
Db 3257 AGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTT 3316
QY 1000 ----- 999
Db 3317 CTGACAGAGAGCCCTTTGGAAGGACTAGAGAAACTCTACAGGAGCCAGAGAGCTGCCT 3376
QY 1000 ----- 999
Db 3377 CCTGAGGAGAGAGCCCGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAAT 3436
QY 1000 -----AGACC 1004
Db 3437 ACTGAGTGGGAAAAAATTGAACCTGCACCTCGCTGACTGGCAGAGAGAAAAATAGATGAGACC 3496
QY 1005 CTTGAAAGACTCCAGGAACCTTCAAGAGGCCACGGATGAGTGGACCTCAAGCTGGCCCAA 1064
Db 3497 CTTGAAAGACTCCAGGAACCTTCAAGAGGCCACGGATGAGTGGACCTCAAGCTGGCCCAA 3556

QY 1065 GCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTTGACTCTCTCCAA 1124
Db 3557 GCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTTGACTCTCTCCAA 3616
QY 1125 GATCACCTCGAGAAAGTCAAGGCATTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACGTG 1184
Db 3617 GATCACCTCGAGAAAGTCAAGGCATTCGAGGAGAAAATTGGCCCTCTGAAAGAGAACGTG 3676
QY 1185 AGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTAT 1244
Db 3677 AGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCATTCAGCTCTCACCGTAT 3736
QY 1245 AACCTCAGCACTCTGGAAGACCTGAAACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAG 1304
Db 3737 AACCTCAGCACTCTGGAAGACCTGAAACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAG 3796
QY 1305 GACCGAGTCAGGCAGCTGCATGAAGCCCAAGGAGCTTTGGTCCAGCATCTCAGCACTTT 1364
Db 3797 GACCGAGTCAGGCAGCTGCATGAAGCCCAAGGAGCTTTGGTCCAGCATCTCAGCACTTT 3856
QY 1365 CTTTCCAGCTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTGCCAAACAAAGTGCCCTAC 1424
Db 3857 CTTTCCAGCTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTGCCAAACAAAGTGCCCTAC 3916
QY 1425 TATATCAACCACGAGACTCAAAACAATTTGCTGGGACCATCCCAAAATGACAGAGCTTAC 1484
Db 3917 TATATCAACCACGAGACTCAAAACAATTTGCTGGGACCATCCCAAAATGACAGAGCTTAC 3976
QY 1485 CAGTCTTTAGCTGACCTGAATAATGTCAAGATTTCTCAGCTTATAGGACTGCCATGAACTC 1544
Db 3977 CAGTCTTTAGCTGACCTGAATAATGTCAAGATTTCTCAGCTTATAGGACTGCCATGAACTC 4036
QY 1545 CGAAGACTGCAGAAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCC 1604
Db 4037 CGAAGACTGCAGAAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCC 4096
QY 1605 TTGGACAGCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTAATAAT 1664
Db 4097 TTGGACAGCACAACCTCAAGCAAAATGACAGCCCATGGATATCCTGCAGATTAATAAT 4156
QY 1665 TGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCT 1724
Db 4157 TGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAAATTTGGTCAACGTCCCT 4216
QY 1725 CTCGCTGGATATGTGTCTGAACCTGGCTGTGATGCTGAAATTTATGATACGGGACGAAACAGG 1784
Db 4217 CTCGCTGGATATGTGTCTGAACCTGGCTGTGATGCTGAAATTTATGATACGGGACGAAACAGG 4276
QY 1785 AGGATCCGTCTCTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAA 1844
Db 4277 AGGATCCGTCTCTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAA 4336
QY 1845 GACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGC 1904
Db 4337 GACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAAGCGC 4396
QY 1905 AGGCTGGGCCCTCTCTCTGATGATTTCTATCCAAATTCAGAGACAGTTGGGTGAAGTTGCA 1964
Db 4397 AGGCTGGGCCCTCTCTCTGATGATTTCTATCCAAATTCAGAGACAGTTGGGTGAAGTTGCA 4456
QY 1965 TCCTTTGGGGCAGTAACATTGAGCCAAAGTGTCGGA 2001
Db 4457 TCCTTTGGGGCAGTAACATTGAGCCAAAGTGTCGGA 4493

RESULT 15

US-10-149-736-41
; Sequence 41, Application US/10149736
; Publication No. US20030216332A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Harper, Scott Q.

; TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
; FILE REFERENCE: UM-06968
; CURRENT APPLICATION NUMBER: US/10/149,736
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/31126
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,848
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 5462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-149-736-41

Query Match 56.6%; Score 1132.2; DB 16; Length 5462;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 373; Indels 202; Gaps 7;

QY	1	GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACAGCTTTAGAAAGAA	60
Db	1199	GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACAGCTTTAGAAAGAA	1258
QY	61	GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAAGGAGAGATTTCTAAT	120
Db	1259	GTATTATCGTGGCTTCTTCTGCTGAGGACACATTCGAAGCACAAGGAGAGATTTCTAAT	1318
QY	121	GATGTGGAAGTGGTGAAGACCAAGTTTCATCTACTCATGAGGGGTACATGATGGATTGACA	180
Db	1319	GATGTGGAAGTGGTGAAGACCAAGTTTCATCTACTCATGAGGGGTACATGATGGATTGACA	1378
QY	181	GCCCATCAGGCGCGGTTGGTAATATTTCTACAATTTGGGAAGTAAGCTGATTGGAACAGGA	240
Db	1379	GCCCATCAGGCGCGGTTGGTAATATTTCTACAATTTGGGAAGTAAGCTGATTGGAACAGGA	1438
QY	241	AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAGA	300
Db	1439	AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAGA	1498
QY	301	TGGGAATGCCTCAGGTAGCTAGCATGGAAGAAACAAAGCAATTTACATAGAGTTTAAATG	360
Db	1499	TGGGAATGCCTCAGGTAGCTAGCATGGAAGAAACAAAGCAATTTACATGCTCCTGGACTG	1558
QY	361	-----GATCTCCAGAATCGAAA-----	360
Db	1559	ACCACTATTGGAGCCTCTCCTACTCAGACCTGTACTCTGGTGACACAACCTGTGGTTACT	1618
QY	361	-----GATCTCCAGAATCGAAA-----	377
Db	1619	AAGGAAACTGCCATCTCCAAACTAGAAATGCCATCTTCTTGATGTGGAGCATAGATTA	1678
QY	378	-----CTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAAGAA	416
Db	1679	CTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCTGGCTTACAGAAGCTGAAACA	1738
QY	417	AGAACAAAGGAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTAAACGCCAA	476
Db	1739	ACTGCCAATGTCTACAGGATGCTACCCGTAAGGAAGGCTCCTAGAAGACTCCAAGGGA	1798
QY	477	GTACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGACAAGTCAGGGTCAATTCT	536
Db	1799	GTAAAAGAGCTGATGAACAATGGCAAGACCTCCAAGGTGAATTTGAAGCTCACACAGAT	1858
QY	537	CTCACTCACATGGTGGTAGTTGATGA-----ATCTAGTGGAGATCACGCA	584
Db	1859	GTTTATCACAACTGGATGAAAACAGGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGAT	1918
QY	585	ACTGCTGCTTTGGAGAACAACACTTAAGG---TATTGGGAGATCGATGGGCAACATCTGT	641
Db	1919	GATGCAGTCTGTTACAAAGACGTTTGGATAACATGAACCTTCAAGTGGAGTGAACCTCGG	1978

QY	642	AGATGGACAGAAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGTCTT	701
Db	1979	AAAAAGTCTCTCAACATTAGGTCCCATTTTGAAGCCAGTTCTGACAGTGAAGCGTCTG	2038
QY	702	ACTGAAGAACAGTGCCTTTTAGTGCAATGGCTTTCAGAAAAAGAAAGATGAGTGAACAAG	761
Db	2039	CACCTTTCTCTGCAGGAACCTTCTGGTGTGGTACAGCTGAAAAGATGATGAATTAAGCCG	2098
QY	762	ATTCACACAACCTGGCTTTAAAGATCAAAATGAATGTTATCAAGTCTTCAAAAACTGGCC	821
Db	2099	CAGGCACCTATTGGAGCGGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCC	2158
QY	822	GTTTAAAGCGGATCTAGAAAAAGAAAAAGCAATCCATGGGCAAACTGTA-----	871
Db	2159	TTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGACTCTCTTGAGACTGTACGA	2218
QY	872	----TTCACCTCAAAACAAGATCTTTTCAACACTGAAGAATAAGTCAGTACCACCCAGAAGA	927
Db	2219	ATATTTCTGACAGAGCAGCCCTTTTGGAAAGGACTAGAGAAACTCTACCAGAGCCACAGAG	2278
QY	928	CGGAAGCATGGCTGA-----TAACCTTCCCGGTGTT	960
Db	2279	CTGCCTCCTGAGGAGAGAGCCCAAGAAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAG	2338
QY	961	GGGATAATTTAGTCCAAAAAATTGAA-----AAGAGTACAGCA	998
Db	2339	GTCAATACTGAGTGGGAAAAAATTGAACTGCACTCCGCTGACTGGCAGAGAAAAATAGAT	2398
QY	999	CAGACCCCTTGAAGACTCCAGGAACCTTCAAGAGCCACGGATGAGCTGGACCTCAAGCTG	1058
Db	2399	GAGACCCCTTGAAGACTCCAGGAACCTTCAAGAGCCACGGATGAGCTGGACCTCAAGCTG	2458
QY	1059	CGCCAAAGCTGAGGTGATCAAGGGATCCTGGAGCCCGTGGCGATCTCCTCATTTGACTCT	1118
Db	2459	CGCCAAAGCTGAGGTGATCAAGGGATCCTGGAGCCCGTGGCGATCTCCTCATTTGACTCT	2518
QY	1119	CTCCAAGATCACCTCGAGAAAAGTCAAGGCACCTTCGAGGAGAAAATTCGCGCTCTGAAAAGAG	1178
Db	2519	CTCCAAGATCACCTCGAGAAAAGTCAAGGCACCTTCGAGGAGAAAATTCGCGCTCTGAAAAGAG	2578
QY	1179	AACGTGAGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCAATTCAGTCTCA	1238
Db	2579	AACGTGAGCCACGTCAATGACCTTGTCTGCCAGCTTACCACCTTTGGGCAATTCAGTCTCA	2638
QY	1239	CCGTATAACCTCAGCACTCTGGAAGACCTTGAACACACAGATGGAAGCTTCTGCAGGTGGCC	1298
Db	2639	CCGTATAACCTCAGCACTCTGGAAGACCTTGAACACACAGATGGAAGCTTCTGCAGGTGGCC	2698
QY	1299	GTCGAGGACCGAGTCAGCAGCTGCATGAAGCCACACAGGGACTTTGGTCCAGCATCTCAG	1358
Db	2699	GTCGAGGACCGAGTCAGCAGCTGCATGAAGCCACACAGGGACTTTGGTCCAGCATCTCAG	2758
QY	1359	CACCTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCCAACAAAGTG	1418
Db	2759	CACCTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCCAACAAAGTG	2818
QY	1419	CCCTACTATATCAACACAGAGACTCAAACTGCTGGGACCATCCCAAAATGACAGAG	1478
Db	2819	CCCTACTATATCAACACAGAGACTCAAACTGCTGGGACCATCCCAAAATGACAGAG	2878
QY	1479	CTCTACCAGTCTTTTAGTGAACCTGAATAATGTCAAGTCTCAGCTTATAGGACTGCCATG	1538
Db	2879	CTCTACCAGTCTTTTAGTGAACCTGAATAATGTCAAGTCTCAGCTTATAGGACTGCCATG	2938
QY	1539	AAACTCCGAAGACTGCAAGAGGCCCTTTGCTGGATCTCTTGGACCTGTGAGTGCATGT	1598
Db	2939	AAACTCCGAAGACTGCAAGAGGCCCTTTGCTGGATCTCTTGGACCTGTGAGTGCATGT	2998
QY	1599	GATGCCTTGGACCCAGCAACCTCAAGCAAAAATGACCAGCCCATGGATATCTGTCAGATT	1658
Db	2999	GATGCCTTGGACCCAGCAACCTCAAGCAAAAATGACCAGCCCATGGATATCTGTCAGATT	3058

Qy	1659	ATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAAC	1718
Db	3059	ATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAAC	3118
Qy	1719	GTCCCTCTCTGCGTGGATATGTGCTGTAAGTGGCTGCTGTAATGTTTATGATACGGGACGA	1778
Db	3119	GTCCCTCTCTGCGTGGATATGTGCTGTAAGTGGCTGCTGTAATGTTTATGATACGGGACGA	3178
Qy	1779	ACAGGGAGGATCCGTGTCCTGCTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACAT	1838
Db	3179	ACAGGGAGGATCCGTGTCCTGCTCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACAT	3238
Qy	1839	TTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAAAGGATTTTGTGAC	1898
Db	3239	TTGGAAGACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAAAGGATTTTGTGAC	3298
Qy	1899	CAGCGCAGGCTGGGCCTCCTTCTGATGATTTCTATCCAAATTCGAAGACAGTTGGGTGAA	1958
Db	3299	CAGCGCAGGCTGGGCCTCCTTCTGATGATTTCTATCCAAATTCGAAGACAGTTGGGTGAA	3358
Qy	1959	GTTGCATCCTTTGGGGCAGTAACATGAGCCAAAGTGTCCGGA	2001
Db	3359	GTTGCATCCTTTGGGGCAGTAACATGAGCCAAAGTGTCCGGA	3401

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 02:48:31 ; Search time 3619.24 Seconds
(without alignments)
16510.166 Million cell updates/sec

Title: US-09-845-416-14_COPY_1000_3000
Perfect score: 2001
Sequence: 1 ggcagttcattgatggagag.....cattgagccaagtgcgga 2001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rod:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gss1:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result	No.	Score	Query Match Length DB ID	Description
1	991	49.5	3870 11 BC036103	BC036103 Homo sapi
2	776.6	38.8	3056 11 AK044536	AK044536 Mus muscu
3	765	38.2	5691 29 AY399453	AY399453 Homo sapi
4	585.2	29.2	728 14 CB228986	CB228986 AGENCOURT

5	571.4	28.6	5697	29	AY399455	AY399455 Mus muscu
6	569	28.4	777	14	CD653550	CD653550 AGENCOURT
7	569	28.4	824	9	AL556247	AL556247 AL556247
8	567.4	28.4	1098	13	BX365572	BX365572 BX365572
9	566.4	28.3	801	14	CB991394	CB991394 AGENCOURT
10	558	27.9	620	13	BQ640063	BQ640063 he23904.Y
11	532.2	26.6	770	12	BG719710	BG719710 602690430
12	511.4	25.6	1298	11	AK087829	AK087829 Mus muscu
13	511.4	25.6	2135	11	AK013510	AK013510 Mus muscu
14	511.4	25.6	4437	11	AK036936	AK036936 Mus muscu
15	511	25.5	797	14	CB960722	CB960722 AGENCOURT
16	509.8	25.5	1384	11	AK075809	AK075809 Mus muscu
17	502	25.1	5676	29	AY399454	AY399454 Pan trogl
18	494.6	24.7	652	10	BB629984	BB629984 BB629984
19	491.6	24.6	704	10	BB610411	BB610411 BB610411
20	489.8	24.5	508	14	CD701871	CD701871 EST18395
21	481.2	24.0	1047	14	CB850319	CB850319 NRA-0070
22	467.2	23.3	854	9	AI196693	AI196693 ui53e10.Y
23	460.6	23.0	3753	11	AK081426	AK081426 Mus muscu
24	457.2	22.8	513	29	CG605968	CG605968 OST283399
25	455.8	22.8	591	13	BX490860	BX490860 DKFZp686F
26	455.8	22.8	717	14	CB527785	CB527785 UI-M-FY0-
27	453.8	22.7	508	29	CG606947	CG606947 OST285335
28	446.2	22.3	542	29	CG594848	CG594848 OST253426
29	439	21.9	578	13	BX485574	BX485574 DKFZp686L
30	436.6	21.8	665	13	BY742604	BY742604 BY742604
31	427.4	21.4	2874	29	AY408546	AY408546 Homo sapi
32	422.8	21.1	898	10	BF182065	BF182065 601804604
33	422.6	21.1	520	29	CG606443	CG606443 OST284316
34	422.6	21.1	2874	29	AY408548	AY408548 Mus muscu
35	420.2	21.0	512	14	CF162938	CF162938 B0718G07-
36	419.4	21.0	488	29	CG597965	CG597965 OST261937
37	417.6	20.9	843	14	CA988247	CA988247 AGENCOURT
38	416	20.8	493	29	CG604818	CG604818 OST280872
39	410.4	20.5	599	10	BB666688	BB666688 BB666688
40	407.2	20.3	554	14	CB613696	CB613696 AMGNNUC:N
41	405.4	20.3	662	12	BJ626491	BJ626491 BJ626491
42	404.4	20.2	493	14	CA888041	CA888041 B0142C06-
43	397.4	19.9	495	14	CA894775	CA894775 B0187G06-
44	397	19.8	595	14	CB177816	CB177816 is21c01.X
45	392.2	19.6	650	13	BY714491	BY714491 BY714491

ALIGNMENTS

RESULT 1	BC036103	3870 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), mRNA (cDNA clone IMAGE:5274415), with apparent retained intron.				
DEFINITION	BC036103.1 GI:23271310				
ACCESSION	BC036103				
VERSION	BC036103.1				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 3870)				
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,				

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257
12477932
2 (bases 1 to 3870)
Strausberg, R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 48 Row: f Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: retained intron.

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5274415"
/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN
Query Match 49.5%; Score 991; DB 11; Length 3870;
Best Local Similarity 99.9%; Pred. No. 6.6e-223;
Matches 1002; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACACAGCTTTAGAACAA 60
Db 1143 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAACACAGCTTTAGAACAA 1202
QY 61 GTATTATCGTGGTCTCTTTCTGCTGAGGACACATTGCAAGCAAGGAGAGATTCTTAAT 120
Db 1203 GTATTATCGTGGTCTCTTTCTGCTGAGGACACATTGCAAGCAAGGAGAGATTCTTAAT 1262
QY 121 GATGTGGAAGTGTGAAAGACCAGTTTCATCTATCATGAGGGGTACATGATGATTTGACA 180
Db 1263 GATGTGGAAGTGTGAAAGACCAGTTTCATCTATCATGAGGGGTACATGATGATTTGACA 1322
QY 181 GCCCATCAGGCGCGGTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 1323 GCCCATCAGGCGCGGTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 1382
QY 241 AAATTATCAGAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCTAAATTTCAAGA 300
Db 1383 AAATTATCAGAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCTAAATTTCAAGA 1442

QY 301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTACATAGAGTTTTTAATG 360
Db 1443 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTACATAGAGTTTTTAATG 1502
QY 361 GATCTCCAGATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAAGA 419
Db 1503 GATCTCCAGATCAGAAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAAGA 1562
QY 420 ACAAGGAAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAAACGCCAAGTA 479
Db 1563 ACAAGGAAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAAACGCCAAGTA 1622
QY 480 CAACAACATAAGGTGCTTCAAGAGATCTAGAACAAAGCAAGTCAGGGTCAATTCTCTC 539
Db 1623 CAACAACATAAGGTGCTTCAAGAGATCTAGAACAAAGCAAGTCAGGGTCAATTCTCTC 1682
QY 540 ACTCACATGGTGGTGTGATGAATCTAGTGGAGATCAGCAACTGCTGCTTTGGAA 599
Db 1683 ACTCACATGGTGGTGTGATGAATCTAGTGGAGATCAGCAACTGCTGCTTTGGAA 1742
QY 600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCGC 659
Db 1743 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCGC 1802
QY 660 TGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGCTTACTTAAAGCGGATCTA 719
Db 1803 TGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGCTTACTTAAAGCGGATCTA 1862
QY 720 TTTAGTGCATGGCTTTTCAGAAAAAGAGATGCAGTGAACAAGATTCACACAACCTGGCTTT 779
Db 1863 TTTAGTGCATGGCTTTTCAGAAAAAGAGATGCAGTGAACAAGATTCACACAACCTGGCTTT 1922
QY 780 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAACTGGCCGTTTTTAAAGCGGATCTA 839
Db 1923 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAACTGGCCGTTTTTAAAGCGGATCTA 1982
QY 840 GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAACAAGATCTTCTTTCAACA 899
Db 1983 GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAACAAGATCTTCTTTCAACA 2042
QY 900 CTGAAGATAAAGTCAAGTACCCAGAACGGAAGCATGGCTGGATAAATTTGCCCGGTGT 959
Db 2043 CTGAAGATAAAGTCAAGTACCCAGAACGGAAGCATGGCTGGATAAATTTGCCCGGTGT 2102
QY 960 TGGGATAATTAGTCCAAAAACTTGAAAAAGAGTACAGCACAGA 1002
Db 2103 TGGGATAATTAGTCCAAAAACTTGAAAAAGAGTACAGCACAGA 2145

RESULT 2
AK044536
LOCUS
DEFINITION
AK044536 3056 bp mRNA linear HTC 20-SEP-2003
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930019F21 product:dystrophin, muscular dystrophy, full
insert sequence.
ACCESSION
VERSION AK044536.1 GI:26090404
KEYWORDS
SOURCE HTC; CAP trapper.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
2
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20499374
11042159
3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20530913
11076861
4

The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.

TITLE
JOURNAL
REFERENCE
AUTHORS

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

TITLE
JOURNAL
REFERENCE
AUTHORS

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216).

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustincich (Department of
Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA
02115, USA) whose assistance is gratefully acknowledged. Please
visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
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/clone="A930019F21"
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GB|NM_007868, evidence: BLASTN, 100%, match=999)"

ORIGIN

Query Match 38.8%; Score 776.6; DB 11; Length 3056;
Best Local Similarity 86.5%; Pred. No. 2.7e-172;
Matches 868; Conservative 0; Mismatches 134; Indels 1; Gaps 1;

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QY 61 GTATTATCGTGGCTTCTTCTGTCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 120

Db 1104 GTACTTTTCATGGCTTCTTCTGCGGAGGATACATTGCGAGCACAAGGAGAGATTTCAAT 1163

QY 121 GATGTGGAAGTGGTGAAGACCAGTTTTCATACTCATGAGGGGTACATGATGGATTTGACA 180

Db 1164 GATGTTGAAGAAGTGAAGAACAGTTTTCATGCTCATGAGGGATTTCATGATGGATCTGACA 1223

QY 181 CCCCATCAGGGCCGGTGGTAAATATTCTACAAATTTGGGAAGTAAGCTGATGGAAACAGGA 240

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QY 241 AAATTATCAGAAGATGAAGAAACTGAAGTACACAGCAGATGAATCTCTTAAATTCAGA 300

Db 1284 AAATTATCAGAAGATGAAGAACTGAAGTGAAGAACAAATGAATCTCTTAAATTCAGA 1343

QY 301 TCGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTTACATAGAGTTTAAATG 360

Db 1344 TCGGAATGCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTTACATAGAGTTTAAATG 1403

QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTTGAATGACTGGCTAACAAAAACAGAAAGAA 419

Db 1404 GATCTCCAGAATCAGAAATTTAAAGAACTAGATGACTGGTTAAACAAAAACTGAAGAGAGA 1463

QY 420 ACAAGGAAAAATGGAGGAAGAGCCTCTTTGGACCTGATCTTTGAAGACCTTAAACCCCAAGTA 479

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QY 480 CAACAACATAAGGTGCTTCAAGGAAGATCTAGAACAAAGAACAAAGTCAAGGTCAATCTCTC 539

Db 1524 CAACAACATAAGGTGCTTCAAGGAAGATCTAGAACAGGAGCAGGTCAAGGTCAACTCGCTC 1583

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Db 1584 ACTCACATGGTAGTAGTGGTTGATGAATCCAGCGGTGATCATGCAACAGCTGCTTTGGAA 1643

QY 600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACACCGC 659

Db 1644 GAACAACCTTAAGGTACTGGAGATCGATGGGCAAAATATCTGCAGATGGACTGAAGACCGC 1703

QY 660 TGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTT 719

Db 1704 TGGATTGTTTTACAAGATATTCTTCTAAATGGCAGCATTTTACTGAAGAACAGTGCCTT 1763

QY 720 TTTAGTGCATGGCTTTTCAGAAAAAGAGATGCAGTGAACAAGATTTCACACAACCTGGCTTT 779

Db 1764 TTTAGTACATGGCTTTTCAGAAAAAGAGATGCAATGAAGAACATTTCAGACAAGTGGCTTT 1823

QY 780 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAATACTGGCCGTTTTTAAAGCGGATCTA 839

Db 1824 AAAGATCAAAATGAAATGATGTCAAGTCTTCAAAAATATCTACTTTAAAAATAGATCTA 1883

QY 840 GAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAAACAGATCTTTCTTCAACA 899

Db 1884 GAAAGAAAAAGCCCAACCATGGAAAAAACTAAGTTCACTCAATCAAGATCTACTTTCCGCA 1943

QY 900 CTGAAGAAATAAGTCAGTGACCCAGAACGGAAGCATGGCTGGATAACTTTTCCCGGTGT 959

Db 1944 CTGAAGAAATAAGTCAGTGACTCAAAAAGATGGAATCTGGATGGAATACTTTGCAACACGT 2003

QY 960 TGGGATAATTAGTCCAAAAAAGCTGAAAAAGAGTACAGCAGACA 1002

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RESULT 3
AY399453
LOCUS
DEFINITION Homo sapiens HCM0229 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY399453 genomic survey sequence.
ACCESSION AY399453
VERSION AY399453.1 GI:39755442
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5691)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 5691)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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Query Match 38.2%; Score 765; DB 29; Length 5691;
Best Local Similarity 89.1%; Pred. No. 1.7e-169;
Matches 894; Conservative 0; Mismatches 0; Indels 109; Gaps 2;
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Db 385 GGCAGTTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTAGAAGAA 444
QY 61 GTATTATCTGCTGCTTCTTCTGCTGAGGACACATTCGCAAGCACAAAGGAGAGATTCTAAT 120
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QY 121 GATGTGGAAGTGGTGAAGAACCCAGTTTCATACTCATGAGGGGTACATGATGGATTGACA 180
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QY 181 GCCCATCAGGCCCGGGTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240
Db 565 GCCCATCAGGCCCGGGTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 624
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Db 625 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTTAATTCAAGA 684
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QY 361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAAGA 419
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QY 420 ACAAGGAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGAAGACCTAAACGCCAAGTA 479
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Db 865 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAACAACTCAGGTCATTTCTCTC 924
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Db 925 ACTCACATGCTGGTGGTAGTTGATGAATCTAGTGGAGATACGCAAACTGCTGCTTTGGAA 984
QY 600 GAACAACCTTAAGGTATTGGGAGATCGATGGGCAAAACATCTGTAGATGGACAGAACCCG 659
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QY 660 TGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGTTTACTGAAGAACAGTGCCTT 719
Db 1045 TGGGTTCTTTTACAAGACATCCTTCTCAAAATGGCAACGTTTACTGAAGAACAG----- 1098
QY 720 TTTAGTGCATGGCTTTTCAGAAAAAAGAAAGATGCAGTGAACAAGATTACACAACCTGGCTTT 779
Db 1099 ----- 1098
QY 780 AAAGATCAAAAATGAAATGTTATCAAGTCTTCAAAAACCTGGCGCTTTTAAAGCGGATCTA 839
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QY 840 GAAAAGAAAAAGCAATCCATGGCAAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 899
Db 1117 GAAAAGAAAAAGCAATCCATGGCAAAACTGTATTCACTCAAAACAAGATCTTCTTTCAACA 1176
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Db 1177 CTGAAGAATAAGTCAGTGACCCAGAGACGGAAGCATGCTGGATAACTTTGCCCGGTGT 1236
QY 960 TGGGATAATTAGTCCAAAAAATTGAAAAGAGTACAGACAGA 1002
Db 1237 TGGGATAATTAGTCCAAAAAATTGAAAAGAGTACAGACAGA 1279
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RESULT 4
CB228986
LOCUS
DEFINITION CB228986 728 bp mRNA linear EST 10-FEB-2003
IMAGE:6884820 5', mRNA sequence.
CB228986
VERSION CB228986.1 GI:28280564
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
1 (bases 1 to 728)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3135 row: e column: 11
High quality sequence stop: 583.
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SOURCE		Mus musculus (house mouse)	
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 5697)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	146711302		
REFERENCE	2 (bases 1 to 5697)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..5697		
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	/mol_type="genomic DNA"		
gene	<1..>5697		
	/locus_tag="HCM0229"		
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Best Local Similarity	77.1%;	Pred. No. 9e-124;	
Matches	773;	Conservative	0; Mismatches 121; Indels 109; Gaps 2
QY	1	GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAAACAGCTTTTAGAAGAA	60
Db	391	GACAGTTCATTGATGGAGACGGAAGTAAATCTGGATAGTTACCAAACTGCTTTTAGAAGAA	450
QY	61	GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTCGAAGCACACAGGAGAGATTTCTAAT	120
Db	451	GTACTTTTCATGGCTTCTTTCTGCCGAGGATACATTCGAGCACACAGGAGAGATTTCAAAAT	510
QY	121	GATGTGGAAGTGGTGAAGACCAGTTTTCATCTACTCATGAGGGGTACATGATGGATTTGACA	180
Db	511	GATGTTGAAGAAAGTGAAGAACACAGTTTTCATGCTCATGAGGGATTCATGATGGATCTGACA	570
QY	181	GCCCATCAGGCGCGGTTGGTAATATTCTACAATTTGGGAAGTAAGCTGATTGGAACAGGA	240
Db	571	TCTCATCAAGGACTTGTGGTAATGTTCTACAGTTAGGAAGTCAACTAGTTGGAAAAGGG	630
QY	241	AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCTAAATTTCAAGA	300
Db	631	AAATTATCAGAAGATGAAGAAAGCTGAAGTCAAGAACAAATGAATCTCTAAATTTCAAGA	690
QY	301	TGGGAATGCCTCAGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG	360
Db	691	TGGGAATGTCTCAGGTAGCTAGCATGGAAAAACAAAGCAAAATTACACAAAGTTCTAATG	750
QY	361	GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAGAAAGA	419
Db	751	GATCTCCAGAATCAGAAATTAAAGAACTAGATGACTGGTTAACAAAAACTGAAGAGAGA	810
QY	420	ACAAAGGAAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTTGAAGACCTTAAAAACGCCAAGTA	479
Db	811	ACTAAGAAAAATGGAGGAAGAGCCCTTTTGGACCTGATCTTTGAAGATCTAAAAATGCCAAGTA	870
QY	480	CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAAGAACAAAGTCAGGGTCAATTTCTCTC	539
Db	871	CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAGGAGCAGGTTCAGGGTCAACTCGCTC	930
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Db 931 ACTCACATGCTAGTAGTGGTTGATGAATCCAGCGGTGATCATGCAACAGCTGCTTGGAA 990
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RESULT 6
LOCUS CD653550 777 bp mRNA linear EST 18-JUN-2003
DEFINITION AGENCOURT 14553000 NIA Human H1 Embryonic Stem Cell cDNA Library
(Long) Homo sapiens cDNA clone IMAGE:30426742 5', mRNA sequence.
ACCESSION CD653550
VERSION CD653550.1 GI:31892067
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 777)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
cDNA Library Preparation: Yulan Piao and Minoru KO
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c lone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM513 row: a column: 23
High quality sequence stop: 715.
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/clone="IMAGE:30426742"
/tissue_type="Embryonic Stem cells"
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library
(Long)"
FEATURES
source
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/note="Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from WiCell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIzol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTT-3'] from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lOne-linker LL-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

ORIGIN

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Query Match 28.4%; Score 569; DB 14; Length 777;
Best Local Similarity 100.0%; Pred. No. 2.2e-123;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1433 CCACGAGACTCAAAACAACCTTGTGGGACCACATCCCAAATGACAGAGCTCTACCACTCTT 1492
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Db 197 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 256

QY 1553 GCAGAGGCGCCCTTGTGGATCTCTTGAGCCCTGTCTAGCTGCATGTGATGCCITGGACCA 1612
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QY 1673 CACTATTATGACCGCCTGGAGCAAGACACAACAATTGGTCAACGTCCTCTCTGCGT 1732
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QY 1733 GGATATGTCTGAACACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 1792
Db 437 GGATATGTCTGAACACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 496

QY 1793 TGTCTGTCTTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTGGAGACAAGTA 1852
Db 497 TGTCTGTCTTTTAAACCTGGCATCATTTCCCTGTGTAAAGCACATTTGGAGACAAGTA 556

QY 1853 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGG 1912
Db 557 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGG 616

QY 1913 CCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCTTTGG 1972
Db 617 CCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCTTTGG 676
```


Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 23 row: 9 column: 04
Seq primer: M13RP1 reverse primer (ABI).

FEATURES

Location/Qualifiers
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/clone_lib="Human Retina cDNA (Un-normalized, unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor
[5'-pGACTAGTTCTAGATCGCGAGCGCGCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 27.9%; Score 558; DB 13; Length 620;
Best Local Similarity 100.0%; Pred. No. 8.1e-121; Mismatches 0; Indels 0; Gaps 0;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AAACAACCTTGCTGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGA 60
QY 1504 ATAATGTCAGATTCTCAGCTTATAGGACTGGCATGGAATCCGAAGACTGCAGAGGCC 1563
Db 61 ATAATGTCAGATTCTCAGCTTATAGGACTGGCATGGAATCCGAAGACTGCAGAGGCC 120
QY 1564 TTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACGACACACCTCA 1623
Db 121 TTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACGACACACCTCA 180
QY 1624 AGCAAAATGACCGCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATG 1683
Db 181 AGCAAAATGACCGCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATG 240
QY 1684 ACCGCCTGGAGCAGACGACACAACAATTTGGTCAACGTCCTCTCTCGTGGATATGTGTC 1743
Db 241 ACCGCCTGGAGCAGACGACACAACAATTTGGTCAACGTCCTCTCTCGTGGATATGTGTC 300
QY 1744 TGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGCTCTT 1803
Db 301 TGAACCTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGCTCTT 360
QY 1804 TTAAAACTGGCATCATTTCCCTGTGTAAGACACATTTGGAAGACAAGTACAGATACCTTT 1863
Db 361 TTAAAACTGGCATCATTTCCCTGTGTAAGACACATTTGGAAGACAAGTACAGATACCTTT 420
QY 1864 TCAAGCAAGTGGCAAGTTCAACAGGATTTTGTACCGCAGCGAGGCTGGGCCCTCTCTTCTGC 1923
Db 421 TCAAGCAAGTGGCAAGTTCAACAGGATTTTGTACCGCAGCGAGGCTGGGCCCTCTCTTCTGC 480
QY 1924 ATGATTCTATCCAAATTCGAAGACAGTTGGTGGAAGTTGCATCCTTTGGGGGCAGTAACA 1983

Db 481 ATGATTCTATCCAAATTCGAAGACAGTTGGTGGAAGTTGCATCCTTTGGGGGCAGTAACA 540
QY 1984 TTGAGCCCAAGTGTCGGA 2001
Db 541 TTGAGCCCAAGTGTCGGA 558

RESULT 11

BG719710 770 bp mRNA linear EST 08-MAY-2001
LOCUS 602690430F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4822807 5', mRNA sequence.

ACCESSION BG719710
VERSION BG719710.1 GI:13998897

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 770)
NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM10731 row: 1 column: 08
High quality sequence stop: 767.

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/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 26.6%; Score 532.2; DB 12; Length 770;
Best Local Similarity 98.1%; Pred. No. 1.1e-114; Mismatches 0; Mismatches 8; Indels 3; Gaps 2;
Matches 560; Conservative 0; Mismatches 8; Indels 3; Gaps 2;
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Db 210 AGCTGACCTGAATATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 269
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Db 390 ACCACTATTATGACCGCTGGAGCAAGACAGACAAATTTGGTCAACGTCCTCTCTGC 449

Qy 1731 GTGGATATGTCCTGAACTGGCTGCTGAATGTTTATGATACGGACGAACAGGGAGGATC 1790

Db 450 GTGGATATGTCCTGAACTGGCTGCTGAATGTTTATGATACGGACGAACAGGGAGGATC 509

Qy 1791 CGTGCTCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAG 1850

Db 510 CGTGCTCTGCTTTTAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAG 569

Qy 1851 TACAGATACCTTTTCAAGCAAGTGCGCAAGTTTCAACAGGATTTGTGACCAGCGGAGGCTG 1910

Db 570 TACAGATACCTTTTCAAGCAAGTGCGCAAGTTTCAACAGGATTTGTGACCAGCGGAGGCTG 628

Qy 1911 GGCCTCCTTCTGCATGATTCTATCCAAATTTCAAGACAGTTGGGTGAAGTTGCATCCTTT 1970

Db 629 GGCCTCCTTCTGCATGATTCTATCCAAATTTCAAGACAGTTGGGTGAAGTTGCATCCTTT 688

Qy 1971 GGGGGCAGTAACATTGAGCCCAAGTGTCGGGA 2001

Db 689 GGGGGCAGTAACATAGAGCCCAAGTGTCGGGA 719

RESULT 12

AK087829

LOCUS

DEFINITION

AK087829 1298 bp mRNA linear HTC 20-SEP-2003

Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330026B12 product:dystrophin, muscular dystrophy, full insert sequence.

AK087829

AK087829.1 GI:26352777

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

REFERENCE

6 (bases 1 to 1298)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/.

FEATURES

Location/Qualifiers

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/note="unnamed protein product; dystrophin, muscular dystrophy (MGD|MGI:94909, GB|NM_007868, evidence: BLASTN, 100%, match=999)

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QY 1973 GGGCAGTAACATTGAGCCCAAGTGTCCGGA 2001

Db 684 GGGCAGTAACATTGAGCCGAGTGTCCAGGA 712

RESULT 14

AK036936

LOCUS

DEFINITION

AK036936 4437 bp mRNA linear HTC 19-SEP-2003

Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930028B14 product:dystrophin, muscular dystrophy, full insert sequence.

ACCESSION

AK036936

VERSION

AK036936.1 GI:26085504

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

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2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

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REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

TITLE

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

JOURNAL

NATURE

AUTHORS

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL

NATURE

REFERENCE

6

(bases 1 to 4437)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

FEATURES

Location/Qualifiers

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Best Local Similarity 93.7%; Pred. No. 1.3e-109;

Matches 533; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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VERSION CB960722.1 GI:30216839
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REFERENCE 1 (bases 1 to 797)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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FEATURES
source

ORIGIN
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Best Local Similarity 99.8%; Pred. No. 1.1e-109;
Matches 522; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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